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GenCore version 5.1.6
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October 1, 2004, 10:03:29; Search time 4879 Seconds (without alignments) 10447.101 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2 143.2 12.2 1335 10 AF23791	AF2379
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143.2 12.2 1338 6 BD0862	86288 G
5 143.2 12.2 1338 10 AV0093	R 075900VA

ALIGNMENTS

mRNA linear ROD 02-SEP-2001 mRNA, complete cds.	Vertebrata; Euteleostomi; thi; Miridae; Murinae; Mus.	g,T.W. inea pig histamine H4 ariation
mRN/	iata, rogne	enber nd gu
	Arssessil Gillstrossa Mus musculus (house mouse) Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.	1 (bases 1 to 1538) Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W. Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation
RESULT 1 AF358859 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE

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ROD 02-SEP-2001
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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841 ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Comparison of human, mouse, rat, and guinea pig l
receptor suggests substantial species variation
Unpublished
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BRPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILCVTKQPALSQNGSVSS
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2. (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
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/note="G-protein-coupled receptor"
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                               organism="Mus musculus"
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                                                                                                                                        Location/Qualifiers
1. .1538
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/protein_id="AAK97381.1"
/db_xref="G1:15420537"
/tb_xref="G1:15420537"
/translation="MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADR
NLTANSNYFFINLA_SDFFVGYDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADR
NLTHRSNYFFINLA_SDFFVGYISIPLYIPHTLFNWFFGSGICMFWLLTDYLLCTASV
YSIVLISYDRYQSVGNAVRYRAQHTGILKIVAQMVAVWILAFLVNGFWILASDSWKNS
TNTEBCEPGFVTEWYILAITAFLEFLLPVSLUVYFSVQIYWSLWKGSLSRCPSHAGF
IATSSRGTGHSREYDTACRTSLPQLEFEDASASLHSESPRGKSSLLVSLRTHMSGSIIAF
KVGSFCRSESPVLHPMSGSIIAGRKLARSLAVLLSAFAICWARYCLFTIVLGYYRRG
ERPKSIWYSIAFWLQWFNSLINPFLYPLCHRRFQKAFWKILCVTKQPAPSQTQSVSS"
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                                                                                                                           81.5%; Score 958.4; DB 10; Length 1593; larity 88.4%; Pred. No. 1.5e-260; Conservative 0; Mismatches 136; Indels 0;
                                                                                                                                       Similarity
                                                                                                                                       Best Local Sim:
Matches 1040;
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Mus musculus chromosome UNK clone RP23-314021, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
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Direct Submission
Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Darkwav. St. Louis, MO 63108, USA
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Sciurognathi; Muridae; Murinae; Mus.
TTCTGCCGATCAGAAAGCCCAGTGCTTCACCAGAGAGCACGTGGAGCTTCTCAGAGGC
                                                        AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA
                                                                                     TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199211 bases at least Q40
Consensus quality: 199561 bases at least Q30
Consensus quality: 199755 bases at least Q20
Insert size: 199000; agarose-fp
Insert size: 199999; sum-of-contigs
Quality coverage: 13.37 in Q20 bases; agarose-fp
Quality coverage: 11.03 in Q20 bases; sum-of-contigs
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McPherson, J.D. and Waterston, R.H.
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Sequencing vector: plasmid; 100%
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Mammalia, Eutheria, Rodentia,
1 (bases 1 to 200346)
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AC131672.2 GI:38194370
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TACCCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGAGAAAG 92940
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   CCATACTGTCTGTTCACAATTGTCCTTTTCAACTTACCCCAGAACGGAACGCCCCCAAATCG
                                                                                                                                                                                                                GIGTGGTACAGCATIGCCTICTGGCTGCAATGGTTCAATTCGTTAATCCCTTTCTG
                                                                                   GGCAGGAAGCTAGCCAGGTCACTGGCCATCCTTCAGCGCTTTTGCCATTTGCTGGGCT
                                                                                                                     CCATACTGTCTGTTCACAATTGTCCTTTCAACTTACCCGCAGAACGGAACGCCCCAAATCG
                                                                                                                                                                                     GTGTGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F. Umland, S.P. and Wang, S.
Polynucleotide encoding a histamine receptor Patent: US 6204017-A 1 20-MAR-2001;
Location/Qualifiers
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Pred. No. 2e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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agudence 1 from patent US 6204017.
AR142850 GI:15104136
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/mol_type="unassigned
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Best Local Similarity 75.1
Matches 886; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.8%; Score 821.4; DB 2; Length 200346; 95.9%; Pred. No. 1.1e-221;
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                                                                                                                               1 56: contig of 56 bp in length
57 156: gap of unknown length
157 1270: contig of 1114 bp in length
271 1370: gap of unknown length
371 85906: contig of 48536 bp in length
907 86006: gap of unknown length
Location/Qualifiers
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/note="assembly_name:Contig16"
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/note="assembly_name:Contig10"
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/note="assembly_name:Contig17"
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromesome="UNK"
/clone="RRP23-314021"
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Matches 843; Conservative
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                                                                                          Score 686.6; DB
Pred. No. 2e-183;
1. .1173
/organism="unknown"
/mol_type="genomic DNA"
                                                                                          Query Match
Best Local Similarity 75.1%;
Matches 886; Conservative
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 TCTTATAGGGCTCAACACACCTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG
                                                                        ATACTGGCTTTCTTGGTAAATGGCCCCGATGATTCTGGCTTCAGGATTCTTGGAAGAACAGC
                                                                                                      421 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA----
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Behan, J.X., Hedrick, J.A., Laz, T.M.,
Umland, S.P. and Wang, S.
Histamine receptor
Patent: US 661353-A 1 02-SEP-2003;
Location/Qualifiers
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US 6613533.
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Sequence 1 from patent
AR391860
AR391860.1 GI:40115588
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Unclassified.
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 5 AR391860 LOCUS

TITLE JOURNAL FEATURES

REFERENCE AUTHORS

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	661 ACCICTTCCAGGACACTACAGAGCTGGGGGGCTTGCAGGACAAGAATT 720 655 GTCTCTCCACACACTCTGGACACTCAGAGGTGACTTCTCAGGAGTCCTT 714 656 GTCTCTCCACACACTCTGGACACTCATCAGAGGACACACTCTCAAGAGATCCTTT 714 657 CTCTCTCCACACACTCTGGACACTCATCAAGAGGACACACAC	RESULT 7 AX139113 LOCUS AX139113 AX130113 AX1301
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TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTAATCCCTTTCTGTAC 1080
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955 TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
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C12N15/00,
A61K37/02,C12N5/00
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llarity 75.1%; Pred. No. 2e-183;
Conservative 0; Mismatches 284;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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JP 2001211889-A/1.
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                                          Length 1173;
                                                                    Indels
                                        Score 686.6; DB 6;
Pred. No. 2e-183;
0; Mismatches 284;
     db xref="taxon:9606"
                                          Query Match 58.4%;
Best Local Similarity 75.1%;
Matches 886; Conservative
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GSECEPGFESEWYILAITSFLEFVIPVILVAYFNMNIYMSIMKRDHLSRCQSHPGLTA
VSSNICGHSFRGRLSSRSLSASTEVPASFHSERQRRKSSLMPSSRTKMNSNITASKM
GSFSQSDSVALHQREHVELLRARLAKSLAILLGVRAVCMAPYSLFTIVLSFSSATG
PKSVWYRIAFWLQWFNSFVNDLLYPLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSST
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/translation="WPDTNST11NLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDK
NLRHRSSYFFIALAISDFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASV
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I (bases I to 1173)

Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dytko, G.M., Mannan, I.J., Boyce, R., Alston, J., Tlerney, L.A., Li, X., Herrity, N.C., Wawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M., Hieble, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R. Cloning, expression, and pharmacological characterization of a movel human histamine receptor

Mol. Pharmacol. 59 (3), 434-441 (2001)
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Direct Submission
Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd.,
       complete
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Pred. No. 2e-183;
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/organism="Homo sapiens"
sapiens histamine receptor
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/db_xref="taxon:9606"
/chromosome="18"
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/product="histamine
                                      AF325356
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|gene="AXOR35"
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Best Local Similarity 75.1%;
Matches 886; Conservative (
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Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M. and Monsma, F.J. Jr.
cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
21104636
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                                                                                                                                                                                                              100) Human Genomics Research, Schering-Plough 2015 Galloping Hill Rd., Kenilworth, NJ 0703
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Monsma,F.J. Jr., Wang,S., Behan,J., Laz,T.M., Greene,J.
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Pred. No. 2e-183;
0; Mismatches 284; Indels 9;
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/organism="Homo sapiens"
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Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A., Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,
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                                                                                 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC
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                                                     TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG
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GSECEPGFFSEWY ILAITSFLEFVI PVILVAY FNNM YWSLMKRDHLSRCQSHPGLTA
VSSNI CGHSFRGRLSSRTSLSASTEVPAS FHSERQRRKSSLMFSRTKMNSNTTASKM
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0; Mismatches 284;
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                                                                                                                                   /note="G protein-coupled
                                                                                                                                                                                                                   /protein_id="AAL09297.1"
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E 1 (bases 1 to 1173)

O'Dowd, B.F.

Discovery of H4, a Novel Histamine Receptor
Unpublished

E 2 (bases 1 to 1173)

S Oyuyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and O'Dowd, B.F.

O'Dowd, B.F.

S Obwd, B.F.

O'Dowd, B.F.

O'Dowd, B.F.

O'Dowd, B.F.

Taddle Creek Rd., Rm. 4353, Toronto, Out M5S 1A8, Canada

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Catarrhini, Hominidae, Homo.
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PA 18840, USA
AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA
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                                             crcargritriccicaagaaccaagargaaracaaracaarrgcrrccaaaargggrrcc
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Puhl, H.L. III, Ikeda, S.R. and Aronstam, R.S. Direct Submission
Submitted (26-UUL-2002) cDNA Resource Center, Institute, One Guthrie Square, Sayre, PA 18840
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Pred. No. 2e-183;
0; Mismatches 284;
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1. 1173
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Matches 886; Conservative
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                                                                    AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA
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| product="histamine receptor H4"
| product="histamine receptor H4"
| product="id=acA083493.1"
| db xref="id:11815245."
| db xref="GOA:09H3N8"
| db xref="GOA:09H3N8"
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| translation="MDDTNSTINLISISTRVILAFFMSLVAFAIMLGNALVILAFVVDK
| NINYLISYSRFINLALSEPFEVGVISIEDYIPHTLEFWDFGKEICVFFMITTDYLLCTASV
| NINYLISYSRFINLALSEPFEVGVISIEDYIPHTLAVFWNMYLAFLVNGPMILVSESWKDE
| GSECGEFERGRALSSRFISASTPYDASFHSERGRRKSSLMFSRTKMNSNTIASKM
| GSFSQSDSVALHQREHVELLRARRLAKSLAILLGGVFAVCWAPYSLFTTVLSFYGSBTG
| PKSVWYRIAFWLQMFNSFVNPLLYPLCHKRFQKAFLKIFCIKKQPLFSQHSRSVS"
 mRNA linear PRI 12-JAN-2002 receptor H4 (HRH4 gene).
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Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2e-183;
0; Mismatches 284; Indels
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                                                                                 H4 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
/cell_line="AML14.3D10"
                                                                                                                                                                                                                  AJ298292.1 GI:18152452
histamine receptor H4; HRH4 gene.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                     Homo sapiens mRNA for histamine AJ298292
                                                                                                                                                                                                                                                                                                                           O'Reilly,M.A.
Identification of a histamine
Role in eosinophil chemotaxis
Unpublished
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Best Local Similarity 75.1%;
Matches 886; Conservative
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HSA298292
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TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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                                   559 rcariciriddaarrcqrqarcccagrcarcrragrcqcrrarrcaacargaararrar
                                                                          TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT
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G protein-coupled receptors
Patent: WO 0185793-A 115-NOV-2001;
PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 686.6; DB 6;
Pred. No. 2e-183;
0; Mismatches 284;
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    .1300
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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AX301229 GI:17382320
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75.1%;
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NETRRSSYFFINLAISDFFWYVISIDFYIPTHCHEMDFGREICVFWLTJDYLLCTASV
YNIVLISYDRYLSVARAVSYRTQHTGVLKIVTLANAWWLAFLVNGPWILVGESKUDS
GSECEPGFFSEWYILAITSFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTA
VSSNICGHSFRGRLSSRRSLSASTEVAFFHSRSTRNESRTROMSNITASKM
GSFSQSDSVALHQREHVELLFRARRLAKSLAILLGVFPVCMAPYSLFTVLSFYSGAT
RKSVWYRIAFMLQMPNDFLIYPLGHRARRLAKSLAILLGVFPVCMAPYSLFTVLSFYSGAT
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RKSVWYRIAFMLQMPNDFLIYPLGHRARPCARRFOKAFLKIFCIKKQPLPSGHSRSVSS"
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product; human TGR62 G-protein coupled receptor (GPCR)"
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Pred. No. 2e-183;
0; Mismatches 284; Indels
                                                                                                                                                       Lin, D.C., Zhao, J., Chen, J.L. and Cutler, G.
Novel receptors
Patent: WO 0200719-A 5 03-JAN-2002;
Pularik Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="REMTREMBL:CAD26818"
                                                                                                                                                                                                                                                                                       /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="GI:19170679"
                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
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Search completed: October 1, 2004, 12:53:50 Job time : 4891 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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8969.266 Million cell updates/sec 1, 2004, 10:03:29 October Run on:

1 atgtcggagtctaacagtac.....accagtcagtatcttcttga 1176 US-10-626-445-5 1176 Title: Perfect score: Sequence:

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3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s;*

SUMMARIES

Description	Aai70981 Mouse his	Aai70982 Rat hista	Aaa46023 Human G p	Aad01124 Human orp	Aaf83203 Human GPC	Aah24007 Human G p	Abz80663 Human his	Abg78739 Nucleotid	Aai 70980 Human his	Abs57063 Human cDN	Aca93262 Human cDN	Abk12959 DNA seque	Aba02496 Human G p	Aah47911 Human G p	Abz42573 Human his	Aad55126 Human H4	Aai66009 Human GPR	Aas98078 Human DNA	Aad55125 Human H4	Aai67750 Human his	Aai70983 Guinea pi	Aad55124 Human H4	Aad55123 Human H4
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ALIGNMENTS

AAI70981 standard; cDNA; 1176 BP RESULT 1 AAI 70981

AAI70981;

(first entry) 18-MAR-2002

Mouse histamine H4 receptor cDNA.

Histamine H4 receptor; mouse; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.

Mus musculus.

WO200192485-A1.

06-DEC-2001.

22-FEB-2001; 2001WO-US005914.

31-MAY-2000; 2000US-0208260P

(ORTH) ORTHO-MCNEIL PHARM INC.

ΰ Liu Lovenberg T, WPI; 2002-114339/15.

P-PSDB; AAM50565.

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

Claim 4; Fig 5A; 92pp; English.

The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The CDNA was isolated from a mouse spleen cDNA library. It shows 72.8% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and ginnea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host calls that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of

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diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and ecrebroviscular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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The present sequence is that of a cDNA clone encoding a rat histamine receptor of the H4 subtype. The CDNA was isolated from a rat spleen cDNA library. It shows 72.5% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor mucleic acid molecules (see AAM170880-83) and polypeptides (see AAM5054-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin 901 AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 961 TACTGTCTGTCACAATTGTCCTTTCAACTTACCCCAGAACGGGAACGCCCCAAATCGGTG 1021 IGGTACAGCATTGGCCTTCTGGCTGCAATGGTTCAATTCGTTTAATCCCTTTCTGTAC CCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGGAAGATACTTTGTGTGACAAAGCAA TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTGTAC New mammalian histamine H4 receptor proteins and polynucleotides ence the proteins, useful in gene therapy for treating diseases where it beneficial to elevate mammalian histamine H4 receptor activity. Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; 1176 CCAGCGCTGTCACAGAACCAGTCAGTATCTTGA BP. Rat histamine H4 receptor cDNA. Claim 4; Fig 5C; 92pp; English. AAI70982 standard; cDNA; 1176 22-FEB-2001; 2001WO-US005914. 31-MAY-2000; 2000US-0208260P. diagnosis; gene therapy; ss (ORTH) ORTHO-MCNEIL Liu C; 2002-114339/15. P-PSDB; AAM50566 WO200192485-A1. Rattus rattus. Lovenberg T,

961 TACTGTTCACAATTGTCC 	AAA46023 standard; CDNA; 1173 B AAA46023; 22-AUG-2000 (first entry) Human G protein coupled recepto Human; G protein coupled reception identification; agonist; screen ss. Homo sapiens.	A 2	12-MAY-1999; 9908-0124351P. 28-MAY-1999; 9908-0136435P. 28-MAY-1999; 9908-0136433P. 28-MAY-1999; 9908-0137127P. 28-MAY-1999; 9908-0137131P. 29-MAY-1999; 9908-0137131P. 29-MAY-1999; 9908-0137131P. 29-SEP-1999; 9908-0155524P. 29-SEP-1999; 9908-0155524P. 29-SEP-1999; 9908-015552P. 29-SEP-1999; 9908-015653P. 10-CCT-1999; 9908-0157280P. 01-CCT-1999; 9908-0157280P. 01-CCT-1999; 9908-0157280P. 01-CCT-1999; 9908-0157281P. 01-CCT-1999; 9908-0157281P. 01-CCT-1999; 9908-0157281P. 01-CCT-1999; 9908-0157281P. 01-CCT-1999; 9908-0157294P. 12-CCT-1999; 9908-0157294P.
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dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other; Suery Match BI.5%; Score 958.4; DB 6; Length 1176; Best Local Similarity 88.4%; Pred. No. 1.2e-289; Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0; ANGROGAGATCTAACAGATCACACATCACAGATCCACAGATCCCTTGGATTT 60 ANGROGAGATCTAACAGACATTGCTATAATGGTAGGCAATGCTCAGATCTTAGCATTT 60 61 TTAATGTCTTCATTTGCTATAATGGTAGGCAATGCTGTGGTCATTTAGCCTTT 120	121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTATTTTTTTT	GCTCAACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG 420	601 IGGGGGTCTGGGGGGGTCTCAGTGGTGTGTGTGTGTGTGTG
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                                                                                                                                                                                                                                                                                                              The present invention describes transmembrane receptors, preferably human grotein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
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inverse or partial agonists useful as therapeutic agents
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Pred, No. 2.4e-204;
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                                Lehmann-Bruinsma K, Chalmers DT, iaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                 Example 1; Page 88-89; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.4%;
Best Local Similarity 75.1%;
Matches 886; Conservative
                                                        Liaw CW, Lin I,
                                                                                                             2000-317986/27.
                                                                                                                                      P-PSDB; AAB02831
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The present sequence is a cDNA encoding hRUP7, an endogenous human orphan by Protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned by RT-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signaling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid expression analysis to provide information about their function in healthy and pathological states
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361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTGTAC
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                                                                       GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA----
                                                                                                          181 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The PFI-013 protein and nucleic acid are useful in the diagnosis and treatment of the above conditions and also for screening drug candidates for the treatment of diseases associated with signal transduction. The antibodies are also useful for enrichment of eosinophils from mammalian, especially human blood and for detecting the
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20-APR-2000; 2000GB-00009973.
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histamine H3 receptor homologue; infection; viral; bacterial; fungal; protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delirium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntingcon's disease; Gilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery; Fitzgerald LR, Graybill TL, 'note= "G protein-coupled receptor" "Human AXOR35" Location/Qualifiers (SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC. 99US-00431898. 2000US-00497790. 26-OCT-2000; 2000WO-US029461 product= 1. .1173 /*tag= a Bergsma DJ, WO200133221-A1 02-NOV-1999; 03-FEB-2000; Homo sapiens 10-MAY-2001 Aubart KM, STANTANT TO COURT OF COURT OF STANTANT AND S

Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma. WPI; 2001-316464/33 P-PSDB; AAB73622

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Michalovich D, Morrow DM,

Claim 2; Page 49-50; 54pp; English

pectoris; myocardial infarction; stroke; ulcers; migraine; voniting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. MXR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR35 activity or expression. Such AXOR35 modulators are particularly useful for treating asthma, and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils or neutrophils in asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosting or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via the detection of mutations in the corresponding gene. AXOR35 proteins are The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to CDNA encoding AXOR35 (AAB74006), and to AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative transmembrane domains and is involved in signal transduction. AXOR35 has homology and structural similarity with G protein-coupled receptors such as the human histamine H3 receptor. The invention also relates to expression vectors and host cells comprising AXOR35 DNA, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia, bulimia, osteoporosis; asthma, allergies; urinary retention; acute heart failure; hypotension; hypertension; angina

also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nuclectides are also useful as diagnostic reagents, in chromosome localisation and tissue expression studies, and for producing transgenic animals useful in drug discovery. AXOR35-specific antibodies are useful for purifying the AXOR35 protein or fragments thereof, and are also useful for trating conditions associated with the expression of the AXOR35 protein. The present 840 180 240 240 300 120 120 180 300 360 360 420 420 480 476 540 534 009 594 9 654 720 714 780 774 834 900 9 9 TTTATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTTT GACTICCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTGTTTAACTGG 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA reretatatatatacatrictecenteacetateatecataceteteatecetete 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC 421 GTGCTGGCCTTCTTAGTGAATGGCCAATGATTTCTAGTTTCAGAGTCTTTGGAAGGA----477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA 541 ATGCTCTTGGAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 661 ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 781 ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC CTCATGTTTTCCTCAAGAACCAAGATGAATAGCAATACAATTGCTTCCAAAATGGGTTCC TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGAGAGTACGCAGAGCTTCTCAGAGGC 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCCTTGGCATTT 1 ArgccagaraciaAragcacaarcaarriarcacraagcacrcgrgrracriragcarrr TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGGTCATCTTAGCCTTT 121 GIGGIGGACAAAAACCITAGACAICGAAGIAGITATITITITITITAGITGGCCAICIT AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTTGG rerraradaacreaacaracredegererreaagarrerrarrerrearderegecerrres 481 ACGAACACAAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA TCATTCTTGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT Greiriceaacarciorodacácicarreadadoradaciarerreadodadarerer rcriscarcasacasacrecriscarcerricarreagasacasasasasasasasas Gaps 6 Length 1173; Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other; Indels Score 686.6; DB 5; Pred. No. 2.4e-204; 0; Mismatches 284; 58.4%; **Čonservative** Similarity Matches 886; 61 61 181 241 301 361 535 715 775 301 361 601 595 655 721 841 Query Match Local 888888888888ò g à 엄 à 셤 à d à d à Db à d ò d ò g ð g ð dd ð g ð d à d à

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                                                                                                                                                                                                                                                                                                                               human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory; anti-asthmatic; anti-aslergic; dermatological; cerebroprotective; stroke; anti-migraine; cardiant; anti-rhumatic; anti-arthritic; antipsoriatic; neuroprotective; inflammation; asthma; allergy; atopic dermatitis; myocardial infarction; migraine; chronic obstructive pulmonary disease; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
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TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAAGGGAACATGTTGAACTGCTTAGAGCC
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The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromatography, in immunoassay of histamine receptor, to identify CDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, wyocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
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The present sequence encodes a human histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian histamine receptor: It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polynucleotide are useful in the treatment and management of disease such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD). Theurathitis, multiple solerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, incsitol phosphate and mitogen activated protein (MAP) kinase), changes in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+mobilization, mitogenic effects, etc
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                                                                                                                                                                                                                                                                               Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
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                   TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGCCCCAAATCGGTG
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                                                                                                                                                                                                                                                                                                                                   Nucleotide seguence of human histamine receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                              ABQ78739 standard; DNA; 1173
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HEDRICK J A.
LAZ T M.
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UMLAND S P.
WANG S.
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                                                                                                                                                                                                                                                                                rggratagaattgcattttggcttcagtggttcaattcctttgtcatccttttgtar
TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC
                                                                                                                        rrcrcccaarcadarrcrgradcrcrrcaccaaaggaacargradactrgcrragagcc
                                                                                                                                                                           AGGAGATTAGCCAAGTCACTCATAGGGGTTTTTGCTGTTTGCTGGGCTCCA
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                                                                                                                                                                                                                                TATTCTCTGTTCACAATTGTCCTTTCATTTTTATTCCTCAGCAACAGGTCCTAAATCAGTT
                                                                   crcargritriccrcaagaaccaagargaaragcaaracaarrgcrrccaaaargggrrcc
                                           ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC
                                                                                                                                                   AGGAAGCTAGCCAGGTCACTGGCCATCCTTTCTGAGCGCTTTTGCCATTTTGCTGGGCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian histamine H4 receptor proteins and polynucleotides the proteins, useful in gene therapy for treating diseases where beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histamine H4 receptor; human; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                  CCAGCGCTGTCACAGAAC --- CAGTCAGTATCTTGA 1176
                                                                                                                                                                                                                                                                                                                                                                                BP.
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 AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, noninsulin dependent diabetes mellitus, hyperglycemia, constipation,
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(see AAM50564-67). The nucleic acids have
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TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               versus host disease; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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20-OCT-2000; 2000US-00693761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aubart KM, Bergsma DJ, Fi
Michalovich D, Morrow DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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The invention relates to an isolated G-protein coupled receptor

C polypeptide, AXOR35, (and its homologues and variants) and its encoding

C polymolectide (and its homologues, variants, complements and RNA

C equivalents). Also included are an anti-AXOR35 antibody, an AXOR35

C equivalents). Also included are an anti-AXOR35 antibody, an AXOR35

C expression vector, producing a recombinant host cell by introducing the

Vector into a cell such that the host cell produces AXOR35, a membrane of

C the host cell expressing AXOR35, identifying/ Screening for agonists or

antagonists of AXOR35 and inhibiting or promoting the function of

C lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,

C administering to the patient AXOR35 agonists or antagonists. The

agonist or antagonist identified is useful for treating a disease such as

C asthma, or for inhibiting or promoting the function of lymphocytes,

C asthma, or for inhibiting or promoting the function of lymphocytes,

C asthmatic lung. AXOR35 or polymucleotide is useful in diagnostic assays,

C or identifying compounds that are agonists or antagonists of AXOR35, as

C vaccines, or for treating infections (Bacterial, fungal, protozoan or

C vaccines, or for treating infections (Bacterial, fungal, protozoan or

C viral infections), transplant rejection, gastrointestinal disorders (such

as gastric ulcer), inflammatory bowel diseases (such as cropic

c irritable bowel syndrome, voniting, inflammation as theumatoid arthritis,

c paciasis), urological diseases (such as rheumatoid arthritis,

c pardiovascular diseases (such as uninary retention),

c ardiovascular diseases (such as uninary retention),

c hypertension, pulmonary disorders (such as treaming),

c hypertension, pulmonary alsoraers (such as renal isoraeries)
                                                     for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease), cough, remal diseases (such as remal ischaemia), arteriosclerosis, atherosclerosis, psychotic and neurological disorders (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence is the CDNA
                                         Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITAIGICCITAGIAGCITITIGCIATAAIGCTAGGAAATGCITIGGICAITITAGCITIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AAITITGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GATITITGGAAAGGAAATCIGITATITITGGCICACIACIGACIATCIGITATGIACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGTCTACAATATTGTCCTCATTAGCTACGATCGATACCAGTTTCAAATGCTGTG
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Pred. No. 2.4e-204;
0; Mismatches 284;
                                                                                                                                      Claim 2; Page 21-22; 24pp; English.
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P-PSDB; ABG71960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding AXOR35
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                                                   ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA
                                                                              -- TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTCGGAATGGTACATCCTTGCCATCACA
                                                                                                                  541 ATGCTCTTGGAATTCCTGCTTCCTGTCTCTGTGGCTTATTTCAATGTACAGATTTAC
                                                                                                                                        TCATICITIGGAATICGIGAICCCAGICAITAGICGCITATITICAACAIGAAITIAI
                                                                                                                                                                               TGGAGCCTGTGGAAGCGTAAGGGCTCTCAGTAGGTGCCTAGCCATGCTGGATTCTCCACT
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CCAGCGCTGTCACAGAAC -- CAGTCAGTATCTTCTTGA 1176
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Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4; hARE-5; hRUP3; hRUP5; hRUP7; hGPCR27; hARE-1; hARE-2; hPPR1; hG2A; hCHN3; hCHN4; hCHN9; hCHN9; hCHN10; hRUF4; signalling cascade.
BP
                                                                 Human cDNA encoding GPCR hRUP7
ACA93262 standard; cDNA; 1173
                                           (first entry)
                                                                                                                                  Homo sapiens
                                           16-JUL-2003
                      ACA93262;
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240

241 AATTITGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 300

GACTICITICAGGIGIGATCICCATICCITIGIACATCCCTCACACGCTGTTCGAATGG

181

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06-JUN-2001; 2001US-00875076

23-JAN-2003

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180

120 120

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The invention relates to a human G protein-coupled receptor (GPCR)

The invention relates to a human G protein-coupled receptor (GPCR)

C appearing as ABU92259-ABU92277 (encoded by CDNAs ACA93256-ACA93274) named

CC hARE-3, hARE-1, hARE-1, hARE-1, hARE-1,

C also included are a plasmid comprising a vector and one of the CDNAs

C above and a host cell comprising the plasmid. The GPCRs are useful for

C the direct identification of candidate compounds as inverse agonists,

C agonists or partial agonists. In vitro and in vivo systems incorporating

CC GPCRs is useful for elucidating and understanding the roles these

C acceptors play in the human condition, both normal and diseased, as well

C as understanding the signalling cascade. The CDNAs are useful for making a

C understanding the signalling cascade. The CDNAs are useful for making a

C understanding the signalling cascade. The CDNAs are useful for making a

C probe for dot-blot analysis against tissue samples. The

C present sequence is a CDNA encoding a GPCR of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel endogenous, orphan, human G protein-coupled receptors useful for identification of modulators of the receptor and as research tools for understanding the role of the receptor in human body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 284;
                                                                                                                                                                                                                                                                                                                                             Lin I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; Page 22; 54pp; English.
         98US-0109213P.
99US-0120946P.
99US-0123946P.
99US-0123946P.
99US-0136437P.
99US-0136437P.
99US-0136437P.
99US-0136437P.
99US-0136437P.
99US-0137127P.
99US-014448P.
99US-014448P.
99US-0146333P.
99US-0156555P.
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75.1%;
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                                                                                                                                                                                                                                                                                                                                             Dang HT,
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Best Local Similarity
                                                                                                                                                                                                                                                                   CHEN R.
DANG H T.
LIAW C W.
LIN I.
                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABU92265
                                                                  12-MAR-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
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TIAATGICITCATITGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT 85 ritargiccriagradcriticcrataargcriagaaargcrirggicarritiagcriri protein coupled receptors of the invention (ABK12957- ABK12964) Score 686.6; DB 6; Length 1266; Pred. No. 2.6e-204; 0; Mismatches 284; Indels 9; Sequence 1266 BP; 317 A; 268 C; 242 G; 439 T; 0 U; 0 Other; ; 0 58.4%; 75.1%; Conservative Similarity 886; 61 Query Match Local Matches à g ò g ò 1134 DNA sequence of human G-protein coupled receptor TGR62 gene. CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173 standard; DNA; 1266 (first entry) 09-APR-2002

ABK12959 ABK12959

BXXXXXB

RESULT 12 ABK12959

Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease; signal transduction modulator; cerebral cavernous malformation; ds; hyperlipidemia; obesity; dyslexia; cardiac mycoma; renal failure; nephritis; hypertension; liver disease; cirrhosis; blood disorder; spleen-associated disorder; immune disorder; gene; chromosome 18p11. New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma. /product= "Human G-protein coupled receptor TGR62" Cutler G; Location/Qualifiers Claim 7; Page 60-61; 78pp; English. 25-JUN-2001; 2001WO-US020363. 23-JUN-2000; 2000US-0213461P. Zhao J, Chen J, . 1195 /*tag= WPI; 2002-147880/19. (TULA-) TULARIK INC P-PSDB; AAU74906 WO200200719-A2 Homo sapiens 03-JAN-2002 Lin DC, Key

The present invention relates to a new G-protein coupled receptor (GPCR)

20 polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRs TGR21, TGR130.1, TGR130.2, human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction.

The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyalexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases such as renal failure, nephritis, nephrotic syndrome, asymptomatic urinary abnormalities, renal tubule defects, hypertension and emphrolishiasis, liver-related disease or condition and emphrolishiasis, liver-related disease or condition and emphrolishiasis, liver-related disease or condition and emphrolishiasis. of the human GPCR nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders or conditions e.g. splenic enlargement, immune disorders, blood disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present nucleic acid sequence is that of the human GPCR TGR62 gene located on chromosome läpil and encodes the human GPCR TGR62 protein of the invention. This sequence encodes one of seven novel G

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This sequence represents a polynucleotide encoding a novel human G protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCRs, protein-coupled receptor (GPCR) designated offer-2067. Like all GPCRs, c nGPCR-2067 has 7 putative transmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant c expression of nGPCR-2067, to antibodies specific for nGPCR-2067, to drug c screening methods that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067 nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants and species homologues and may also be used in C 2067 allelic variants and species homologues and may also be used in nucleic acids in screening for a predisposition to nGPCR-2067-associated c nucleic acids may additionally be used to generate transgenic nucleic acids may additionally be used to generate transgenic animals, including knockout animals, which may provide an insight into treating a variety of human disorders, and may also be used in the design of antisense molecules for suppressing expression of nGPCR-2067 in cells. C nGPCR-2067, and nGPCR-2067 modulators may be used to treat a wide variety of medical conditions, particularly mental disorders, central nervous system diseases, and metabolic diseases. Diseases that may be treated
                                                                                                                                                                                                                              Human, nGPCR-2067; G protein-coupled receptor; 7TM receptor;

Mignal transduction; mental disorder; central nervous system disease;

Mignal transduction; mental disorder; central nervous system disease;

Migral transduction; milection; HIV-1; HIV-2; pain; neurological disorder;

Migralia; depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;

Migraliason; disease; proliferative disorder; ancer; psorlasis;

Migraliason; proliferative disorder; dementia; Alzheimer's disease;

Migraliason; proliferative disorder; dementia; Alzheimer's disease;

Migraliason; proliferative disorder; dementia; hypertension;

Migraliamatory conditions; dautoimmune disorder; rheumatoid arthritis;

Migraliabetic; metabolic; hypertensive; hypotension;

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                                                                                                                                                                              Human G protein-coupled receptor nGPCR-2067-encoding DNA.
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  include viral infections, particularly HIV-1 or HIV-2 infections; pain, central nervous system, neurological and psychotic disorders such as Huntington's disease, schizophremia, migraine, depression, anxiety, bipolar disorder, dementia, Alzheimer's disease, and Parkinson's disease, proliferative disorders such as cancers, benign prostatic hypertrophy and psoriasis; metabolic disorders such as diabetes, dyslipidaemia, obesity, and anorexia; thyroid disorders; cardiovascular diseases such as hypertension, hypertension, thrombosis, mycocardial infarction, cardiomyopathies, and atheroscierosis; inflammatory conditions; autoimmune disorders (e.g., rheumatoid arthritis); hormonal disorders;
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                                                                                                                                                                                                                                                                                                                    IGGIACAGCAITGCCTICIGGCIGCAAIGGIICAAITCGIITGIIAAICCCIITCIGIAC 1080
                                                                                                                                                                                                                                                             TATTCTCTGTTCACAATTGTCCTTTCATTTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATTGTGTCACAAGCGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAAGCAA 1174
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altering intracellular cAMP concentration;
regulating signal transduction; ss.
TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human G protein-coupled receptor protein BG26 encoding cDNA
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Disclosure; Fig 1; 523pp; English
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The protein is applicable as a tool in screening ligands or drug candidates for regulating signal transduction from such protein treating diseases associated with its abnormality
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                                                                                                        Sequence 1312 BP; 326 A; 276 C; 251 G; 459
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Matches 886; Conservative
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the
                                                                                                                                                                                                       1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; arcentared disease; cell regeneration-related disease; slos; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; pstaft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; hyper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccatigidicacaadgccttcaaaadgctttcttgaaaatattttgtataaaaaggcaa
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presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related desases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune disease, e.g. ADS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crobh's disease, diabetes, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or ny other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42521 to ABZ42869 encode GPCR proteins given in ABP83675 to ABP825018, which are used in the exemplification of the present invention
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Sequence 3689 BP; 975 A; 739 C; 746 G; 1229 T; 0 U; 0 Other;

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o 815 TCTGCATCGACAGAAGTTCCTGCATCCTTTCATTCAGAGAGAG	781 AICTGGTGTCTTPAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC	o 875 CTCATGITITCCTCAAGAACCAAGAATAGCAATACAAITGCTICCAAAAITGGGITCC	841 TICTGGGATGGGAAAGTGCAGGGCTTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC	935 TICTCCCAATCAGATTCTGTAGCTCTTCACCAAAGGGAACATGTTGAACTGCTTAGAGCC	901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGGTGGGCTCCA	995 AGGAGATTAGCCAAGTCACTGGCCATTCTCTAGGGGTTTTTGCTGTTTGCTGGGCTCCA	961 TACTGTCGACAATTGTCCTTTCAACTTACCCCAGAACGCACAATCGGTG	1055 TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGT	1021 IGGTACAGCATTGCCTTCTGGCTGCAATGGTTTGTTTTGT	1115 TGGTATAGAATTGCCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT	1081 CCTTTGTGTCACAGGCGTTTCCAGAAGGGTTTCTGGAAGATACTTTGTGTGACAAAAGCAA	1175 CCATTGTGTCACAAGCGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGCAA	1141 CCAGCGCTGTCACAGAACCAGTCAGTATCTTGA	1235 CTCTACCATCACAACACAGTCGGTCAGTATCTTTAA	
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 8, Appl	Sequence 6. Appl	. 9	14		Sequence 1170	Seguence 1, Appl		14		2	Sequence 2. Appl	1	14	14	8	121	Sequence 22, A	
US-08-767-993-8	US-08-313-553-6	US-08-767-993-6	US-09-016-434-1411	US-09-976-594-158	US-09-016-434-1170	US-08-461-812-1	US-09-371-705-1	US-08-232-463-14	US-08-875-540-2	US-09-171-456-2	US-09-473-634-2	US-08-103-170-1	US-08-875-540-14	US-09-473-634-14	US-09-171-456-18	US-09-016-434-1217	US-08-349-696-22	
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56	56	56	55.2	53.6	51.6	51.6	51.6	49.4	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	48.4	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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US-09-414-010-1

Sequence 1. Application US/09414010

Patent No. 6204017

GENERAL INFORMATION:

APPLICANT: Behan, Jiang Xu

APPLICANT: Hedrick, Joseph A.

APPLICANT: Monas M.

TILE DF INVENTION: Histamine receptor

TILE DF INVENTION: Histamine receptor

TILE OF INVENTION: Histamine receptor

TILE OF INVENTION: Histamine receptor

CURRENT APPLICATION NUMBER: US/09/414,010

CURRENT APPLICATION NUMBER: US/09/414,010

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 1

LENGTH: 1173

TYPE: DNA

US-09-414-010-1
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Length	Indels
DB 3;	284;
Score 686.6; Pred. No. 2.96	0; Mismatches
Query Match 58.4%; Score 686.6; DB 3; Length 1173; Best Local Similarity 75.1%; Pred. No. 2.96-208.	Matches 886; Conservative

	1 AIGCAGATACTAATAGCACAATTTATCACTAAGCACACTGGTTACTTTAGCATTT 60	09
	61 TTAGGECTTAGGAGCTTTGCTAGAAAGGAAGGAATGCTGTGTGTCTTAGCTTT 120	120
Qy 12: Db 12:	121 GIGGIGGACAGAAACTTAGACATGAAGTAATTATTTTTTTTTT	180
Oy 181 O	181 GACTICCICGIGGGIITGAITTCCATICCICGIACAICCCICACGIGITGITTAACIGG 240	240
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Patent No. 6613533
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Wonsma, Frederick J. Jr.
APPLICANT: Wang, Skelley L.
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Pred. No. 2.9e-208;
0; Mismatches 284;
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.1%;
Matches 886; Conservative 0
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CORGANISM: Homo sapiens
US-09-812-216-1
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 143.2; DB 3;
Pred. No. 3e-35;
0; Mismatches 278;
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REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09165543
Patent No. 6093545
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TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
'ENGTH: 1338 base pairs
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
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                         NAME: Elizabeth A. Hanley
REGIGSTRATION UNDRER: 33.505
REFRENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.7)227-7400
TELEPHONE: (6.7)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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RESULT 5
US-08-985-030-3
Sequence 3, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:

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APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
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REGISTRATION NUMBER: 39,030
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TELECOMMUNICATION INPORMATION:
TELEPAX: (617)227-740
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
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APPLICANT: Erlander, Mark
APPLICANT: Payeri, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:CDNA
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CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
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Best Local {
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                                                         474 GAACAGCACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCAC
                                                                                                 540 CAGCICCATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCAT
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Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
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Pred. No. 2.3e-34;
0; Mismatches 286;
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REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: LAHIVE & COCKFIELD, LLP
28 State Street
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APPLICATION NUMBER: 09/042,780
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53.6%;
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Best Local Similarity 53.6°
Matches 341; Conservative
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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STREET: 20
TTV: Boston
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LOCATION:
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; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Exlander, Mark
; APPLICANT: Exlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Pyati, Jayashree
; APPLICANT: Pyati, Jayashree
; TITLE OF INVENTION: BUBTYPE
; TITLE OF INVENTION: SUBTYPE
; TITLE OF STOUGHOUS-21
; CURRENT APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEGTWARE: PATENTIN VET. 2.0
; SEQ ID NOS: 8
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Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286;
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US-09-642-514-6
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APPLICANT: Exlander, Mark
APPLICANT: Briander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Anne
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SSCTARRE: Patentin Ver. 2.0
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                                                                             Length 1335;
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11.9%; Score 140.4; DB 4;
Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286;
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Patent No. 6413743
GENERAL INFORMATION:
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US-09-642-855-6
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
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Pred. No. 3.5e-34;
0; Mismatches 286;
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Patent No. 6093545
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2689 base pairs TYRE: nucleic acid STRANBENESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
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Best Local Similarity 53.6%;
Matches 341; Conservative
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291..1625
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; LOCATION:
US-08-985-090-1
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US-09-165-543-1
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APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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APPLICATION NUMBER: US/08/985,090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MR-n-CURPER: Patentt
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Patent No. 5885893
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RECISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNJ
TELECOMMUNICATION INFORMATION;
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APPLICANT: Lovenberg, Mark
APPLICANT: Lovenberg, Mark
APPLICANT: Evlander, Mark
APPLICANT: Fyati, Jayashree
APPLICANT: Huvar, Arne
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF 1
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT PILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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US-09-167-354-5
Sequence 5, Application US/09167354A
; Patent No. 6136559
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Pred. No. 3.5e-34;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/165,543 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 2689 base pairs
TYPE: nucleic acid
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LOCATION:
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US-09-165-543-1
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US-09-642-514-5
; Sequence 5, Application US/09642514
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APPLICANT: Evander, Mark
APPLICANT: Part, Jayashree
APPLICANT: Part, Jayashree
APPLICANT: Part, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
ITILE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
FRIOR APPLICATION NUMBER: 09/167,354
FRIOR APPLICATION NUMBER: 09/167,354
FRIOR APPLICATION NUMBER: 09/167,354
FRIOR SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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US-09-642-855-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 140.4; DB 4; Length 53.6%; Pred. No. 3.5e-34; Live 0; Mismatches 286; Indels
                                                                                                                     594 GATTTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
                                                                                                                                                      958 carctacrdacarcadagececaccitece 993
                                                                                                                                                                                                                                              Sequence 5, Application US/09642855 Patent No. 6413743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 53.69
Matches 341; Conservative
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5
LENGTH: 2699
                                                                                                                                                                                                                              -09-642-855-5
                                                     534
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474 GAACAGCACGAACACAAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCAC 533
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APPLICANT: Lovenberg, Timothy
APPLICANT: Exlander, Mark
APPLICANT: Fraid axis, Aris
APPLICANT: Fyati, Jayashree
APPLICANT: Payel, Jayashree
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORILOS
CURRENT APPLICATION NUMBER: US/09/642,514
PRIOR APPLICATION NUMBER: US/09/642,514
PRIOR PRILING DATE: 2000-08-21
PRIOR PRILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
TEMORY. 2.0
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Best Local Similarity 53.6%; Pred. No. 3.5e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9;
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US-09-642-514-5
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GAACAGCACGAACACAAAAGGACTGTGAGCCTTTGTTACAGAGTGGTACATCCTCAC 533
                                                                       838 CAGCTCCATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCAT 897
                                                                                                                 534 CATTACAATGCTCTTGGAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACA 593
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Pred. No. 1.2e-19;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                     594 GAITTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
                                                                                                                                                                                                                    958 chrchactrehachrcadadddacaccaccrccd 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATLORUB JOACH AND SILVETI REGISTRATION NUMBER: 39,030 REGISTRATION NUMBER: 39,030 REGISTRATION NUMBER: 39,030 TELEPHONE: (617)722-7400 TELEPHONE: (617)722-7424 INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS: LENGTH: 1086 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08985090 Patent No. 5885893
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ilarity 54.6%;
Conservative
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & CO
STRET: 28 State Stree
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
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STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 212; Conserv
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US-08-985-090-6
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US-08-985-090-6
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October 1, 2004, 12:53:59 ; Search time 659 Seconds (without alignments) 9046.754 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3340653 seqs, 2534783454 residues
                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1. Application US/09812216
Patent No. US20020098539A1
GENEAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Behan, Jiang Xu
APPLICANT: Behan, Jiang Xu
APPLICANT: Monsan, Frederick J. Jr.
APPLICANT: Monsan, Frederick J. Jr.
APPLICANT: Monse, Kelley L.
APPLICANT: Wang, Suke
ITLE OF INVENTION: Histamine receptor
FILE OF INVENTION: Histamine receptor
FILE OF INVENTION: Histamine receptor
FURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET. 2.1

seribution.	Description	Sequence 1, Appli			Segmence 13, Appl		יי ר ייר	7.		, ,	1:	ή,		, i	sequence 5, Appli
	SUMMARIES	US-09-812-216-1	US-10-340-411-1	US-09-875-076-13	US-09-876-252-13	US-10-052-193-1	US-10-272-983-13	US-10-354-769-1	US-10-393-807-13	US-10-417-820A-13	US-10-723-955-13	IIS-10-737-619-1	TIS 10 767 52	TIS-09-891-1388-E	C-WOCT-T/0-C0 C0
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,	% Query Match Length DB	1173	1173	1173	1173	1173	1173	1173	1173	1173	1173	1173	1173	1266)
	% Query Match	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	
	Score	686.6	686.6	9.989	9.989	9.989	9.989	9.989	9.989	9.989	9.989	9.989	686.6	686.6	
	Result No.	77	9	4	Ŋ	9	7	α ·	o i	10	11	12	13	14	

61 TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGGTGGTCATCTTAGCCTTT 120

1 AIGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCCTTGGCATTT 60

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Query Match
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9;

ORGANISM: Homo sapiens

US-09-812-216-1

LENGTH: 1173

SEQ ID NO 1 TYPE: DNA 1 Argccagaractaaragcacaarcaartrarcactaagcactcgrgtractraagcartr

9

Gaps

6

equence 1 equence 1 equence 6 equence 2	0.425	226,6	equence 4, equence 4, Sequence 4, Sequence 3, equence 3,	1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	1, 9 1, 6 5,
09-852-165-1 10-225-5678-1 10-225-5678-1 10-290-078-2	S US-10-290-07 7 US-10-398-03 3 US-09-891-05 3 US-09-891-05 US-09-350-206	US-09-345 US-09-166 US-10-28 3 US-09-89 2 US-10-15	0-206 9-755 6-334 6-334 0-255 9-755	US-09-166-334 VS-10-282-95 VS-10-282-95 US-09-891-05 US-09-350-206 US-09-349-755	. US-09-166-334-1 5 US-10-282-958-1 5 US-10-225-567A-548 7 US-10-727-021-5 7 US-10-283-975A-697
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ALIGNMENTS

JS-09-812-216-1

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541 AIGCTOTIGGAATTCCTGCTTCTCTGTGGGCTTATTTCAATGTACAGATTTAC 600
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APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiachong
APPLICANT: Li, Xiachong
APPLICANT: Li, Xiachong
APPLICANT: Michalovich, David
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: G970655-2C1
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT APPLICATION NUMBER: 09/693,761
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-20-03
PRIOR PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRAESQ for Windows Version 4.0
SEQ ID NO: 1
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Pred. No. 2e-209;
0; Mismatches 284;
                                ; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
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Best Local Similarity 75.1%;
Matches 886; Conservative (
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ORGANISM: Homo sapien
                                                                                    GENERAL INFORMATION:
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Sequence 1, Application US/10349253A

GENERAL INFORMATION:

APPLICANT: Aubart, Kelly

APPLICANT: Bergsma, Derk

APPLICANT: Graybill, Todd

APPLICANT: Li, Xiatong

APPLICANT: Li, Xiatong

APPLICANT: Li, Xiatong

APPLICANT: Michalovich, David

APPLICANT: Morrow, Dwight

ITILE OF INVENTION: AXCN35, A G-Protein Coupled Receptor

ITILE OF INVENTION: AXCN35, A G-Protein Coupled Receptor

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ORGANISM: Homo sapien
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      Length 1173
Query Match
58.4%; Score 686.6; DB 13; Length
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels
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                                 Score 686.6; DB 13; Length 1173;
Pred. No. 2e-209;
0; Mismatches 284; Indels 9;
                                     Query Match
Best Local Similarity 75.1%;
Matches 886; Conservative
; ORGANISM: Homo sapiens
US-09-875-076-13
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Pred. No. 2e-209;
0; Mismatches 284; Indels
       PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR APPLICATION NUMBER: 60/156,634
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NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATEUTIN VETSION 3.0
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Best Local Similarity 75.1%;
Matches 886; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Lin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled I
                                                                                                                                                CCTTTGTGTCACAGGGGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGGAA 1140
                                                TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTGTAC 1080
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CURRENT FILING DATE: 2001-06-07

PRIOR PAPELICATION NUMBER: 09/416,760

PRIOR PILING DATE: 1999-10-12

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-11-27

PRIOR PELING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR PELING DATE: 1999-02-26

PRIOR PELING DATE: 1999-02-26

PRIOR PELING DATE: 1999-02-26

PRIOR FILING DATE: 1999-03-12

PRIOR PELING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR PELING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR APPLICATION NUMBER: 60/137,131
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09876252
Publication No. US20030018182A1
GENERAL INFORMATION:
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FILING DATE: 1999-05-28
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; Bublication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pitzer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; TILE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; TILE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2e-209;
0; Mismatches 284;
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Best Local Similarity
Matches 886; Conserv
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Pred. No. 2e-209;
0; Mismatches 284; Indels 9;
                                                                    APPLICANT: Chen, Ruoping
APPLICANT: Dang, Houng T.
APPLICANT: Dang, Houng T.
APPLICANT: Lin, Chen
APPLICANT: ARENGOSO
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 1990-10-17
FRIOR APPLICATION NUMBER: 60/109,213
FRIOR APPLICATION NUMBER: 60/109,213
FRIOR APPLICATION NUMBER: 60/120,416
FRIOR APPLICATION NUMBER: 60/120,416
FRIOR FILING DATE: 1999-02-26
FRIOR PELING DATE: 1999-02-12
FRIOR APPLICATION NUMBER: 60/123,946
FRIOR PILING DATE: 1999-03-12
FRIOR PILING DATE: 1999-03-12
FRIOR PILING DATE: 1999-03-12
FRIOR PILING DATE: 1999-05-28
FRIOR PILING DATE: 1999-05-28
FRIOR PILING DATE: 1999-05-28
FRIOR FILING DATE: 199
Sequence 13, Application US/10272983
Publication No. US20030148450A1
                    GENERAL INFORMATION:
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Best Local Similarity 75.1%;
Matches 886; Conservative
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1075 CCATTGTGTCACAAGGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGGCA 1134
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421 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAGGA---- 476
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APPLICANT: O'Reilly, Mark A.
APPLICANT: Perer, Beate
TILE OF INVERTION: NOVEL POLYPEPTIDE
FILE REFERENCE: PC10373B
CURRENT APPLICATION NUMBER: US/10/354,769
CURRENT APPLICATION NUMBER: US 09/698,801
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-6-14
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-66-14
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-60-20
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Publication No. US20030149242A1
GENERAL INFORMATION:
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1075 CCATTGTGTCACAAGGGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGCAA 1134
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APPLICANT: Dang, Huong T.
APPLICANT: Lin, PRORMANTION:
APPLICANT: Lin, 1-Lin
TILLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REPRENCE: ARRNO'05
FUE REPRENCE: ARRNO'05
CURRENT PILING DATE: 2003-03-21
FRIOR APPLICATION NUMBER: US/10/9417,044
PRIOR PELING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-38
PRIOR FILING DATE: 1999-0
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                                                                                                                                              895 AGGAGATTAGCCAAGTCACTGGCCATTCTTTAGGGGTTTTTGCTGTTTGCTGGGCTCCA
                                          TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCCAGAACGGAACGCCCCCAAATCGGTG
                                                                   TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTAATCCCTTTCTGTAC
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Pred. No. 2e-209;
0; Mismatches 284; I
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Publication No. US20030175891A1
GENERAL INFORMATION:
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Best Local Similarity 75.1%;
Matches 886; Conservative (
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Pred. No. 2e-209;
0; Mismatches 284; Indels
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Best Local Similarity 75.1%;
Matches 886; Conservative
                   SOFTWARE: PatentIn version
                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1
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APPLICANT: Liaw, Chen W.
APPLICANT: Chalmers, Derk T.
APPLICANT: Chalmers, Derk T.
APPLICANT: Chalmers, Derk T.
APPLICANT: Chen, Roceptor C.
ITILE OF INVENTION: Constitutively Activated Human G Protein Coupled
ITILE OF INVENTION: Roceptor C.
ITILE OF INVENTION: UNMER: 05/10/416, 760
FRIOR PELING DATE: 1999-10-13
FRIOR PELING DATE: 1999-10-13
FRIOR APPLICATION NUMBER: 60/110, 060
FRIOR FILING DATE: 1998-11-20
FRIOR PELING DATE: 1998-11-20
FRIOR PELING DATE: 1998-11-20
FRIOR PELING DATE: 1999-02-26
FRIOR APPLICATION NUMBER: 60/123, 945
FRIOR PELING DATE: 1999-03-12
FRIOR FELING DATE: 1999-03-13
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Pred. No. 2e-209;
0; Mismatches 284; Indels 9;
                                                         ; Sequence 13, Application US/10417820A; Publication No. US20030229216A1; GENERAL INFORMATION:
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Best Local Similarity 75.1%;
Matches 886; Conservative (
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lian, T.Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruinsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Wartin
APPLICANT: Core, Martin
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TITLE OF INVENTION: Receptors
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CURRENT APPLICATION NUMBER: US/10/723,955

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 10/417,820

PRIOR PILING DATE: 2003-4-16

PRIOR PILING DATE: 2003-4-16

PRIOR PILING DATE: 1999-10-12

PRIOR PILING DATE: 1999-10-13

PRIOR PILING DATE: 1999-0-16

PRIOR PILING DATE: 1999-0-2-16

PRIOR PILING DATE: 1999-0-2-16

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Best Local Similarity 75.1
Matches 886; Conservative
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	QY 121 GTGGTGGACAGAAACCTTAGACATGAAGTAATTTTTTTTT	QY 181 GACTICCTCGTGGGTTTGATTCCTCTGTACATCCCTCACGTGTTGTTTAACTGG 240 Db 181 GACTICTTGTGGGGTCTGATCCCTTGTACATCCCTCACACGCTGTTCGAATGG 240	QY 241 AATTITGGAAGTGGAATCTGCALGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 300	Qy 301 TCTGTCTACAATATTGTCCTCATTAGCTACGATACCAGTCAGT	QY 361 TCTTATAGGGCTCAACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGTGGTGTTTGG 420 Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420	QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGGTTCTGGAAGAACAGC 480	OY 481 AGGAACACAAAGGCTGGCCTGGCTTGTTACAGAGTGGTACATCCTCACCATTACA 540 Db 477TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA 534	QY 541 AIGCICTIGGAAITCCIGCTICCTGIGGCTTAITTCAAIGIACAGAITTAC 600 Db 535 ICAITCIIGGAAITCGIGAICCCAGICAICTIAGICGCTTAITTCAACAIGAAIAITAI 594	QY 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660	QY 661 ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGGGGGGGG	OY 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCCTCGAAGAAAGA	QY 781 ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC 840	OY 841 TICIGGGGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTICTCAGAGGC 900	OY 901 AGGAGGTAGCCAGGCATCCTTCTGAGGCTTTTGCCATTTGCTGGGGTCCA 960	OY 961 TACTGTCTGTCAAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020	Qy 1021 IGGIACAGCAITGCCTCTGGCTGCAATGGTICAAITGGTIAAICCCTITCTGIAC 1080	Qy 1081 CCTTGGGGGGGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140	Oy 1141 CCAGCGCTGTCACAGAACCAGTCAGTATCTTGA 1176
Db 535 TCATTCTTGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594	Qy 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660	A CONTROL CONTROL CONTROL CAGA CONTROL CAGA CONTROL CAGA CAGA CAGA CAGA CAGA CAGA CAGA CAG	Oy 721 CCTGGATTGAAGAATCAGCTGCATCACAGAAAGTCCTCGAAGAAAGA	QY 781 ATCTGGTGTCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC 840	QY 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC 900	Qy 901 AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCAGTTCCA 960	Qy 961 TACTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGCCCCCAAATCGGTG 1020	Oy 1021 TGGTACACATTGCCTTCTGGCTGCAATGGTTCAATTGGTTAATCCTTTGTGTAC 1080	Qy 1081 CCTTGFGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTGFGTGACAAAGCA 1140	Qy 1141 CCAGCGCTGTCACAGAACCAGTCAGTATCTTCTGA 1176	RESULT 12 US-10-737-619-1	Sequence 1, Application 05/10/5/619 GENERAL INFORMATION: APPLICATION: Histor, Inc. TITLE OF INTENTION: HIGHWAIN PROPERTOR NAME OF TAMES.	FILE REFERENCE: PC10963A CURRENT APPLICATION NUMBER: US/10/737,619 CURRENT FILING DATE: 2003-12-16 PRIOR APPLICATION NUMBER: 0103-13-16	PRIOR FILING DATE: 2001-01-17 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.1 SEO ID NO.1) LENGTH: 1173 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-737-619-1	58.4%; Score 686.6; DB 17; Length 1173; milarity 75.1%; Pred. No. 26-209; Conservative 0. Mismarches 284. Indels 0.	1 ATGTCGAGITTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCATTT 60	1 ALGCCAGATACTAATAGCACTAATCAATTATCACTAAGCACTCGTGTTACTTTAG 61 TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAG

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TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG
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APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. U920030083245Alel Receptors
FILE REFERENCE: 018781-006210US
CURRENT APPLICATION NUMBER: US/99/891,138A
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR FILING DATE: 2000-06-23
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APPLICANT: Lin, Daniel Chi-Hong APPLICANT: Zhao, Jiagang
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US-09-891-138A-5
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
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                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
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Pred. No. 2e-209;
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/782,596
CURRENT APPLICATION NUMBER: US/10/782,596
CURRENT APPLICATION NUMBER: US/09/875,076
PRIOR APPLICATION NUMBER: US/09/875,076
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
                                                                                                            Sequence 13, Application US/10782596
Publication No. US20040137509A1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 886; Conserv
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ORGANISM: Homo sapiens
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Pred. No. 2.1e-209;
0; Mismatches 284; Indels 9;
                                                                                                                                                                      LOCATION: (25)..(1197)
COTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-5
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75.1%;
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Best Local Similarity 75.19
Matches 886; Conservative
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
             SOFTWARE: Pater
SEQ ID NO 5
LENGTH: 1266
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Pred. No. 2.1e-209;
0; Mismatches 284;
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| Publication No. US20030032784A1 |
| GENERAL INFORMATION: |
| APPLICANT: Lind, Peter |
| APPLICANT: Lind, Peter |
| APPLICANT: Sejlitz, Torsten |
| APPLICANT: Wogeli, Gabriel |
| APPLICANT: Wogeli, Gabriel |
| APPLICANT: Wogeli, Gabriel |
| APPLICANT: Wogeli, Gabriel |
| APPLICANT: Wodel, Linda S. |
| TITLE OF INVENTION: No. US20030032784A1el G F |
| FILE REFERENCE: 00231regUS |
| CURRENT FILING DATE: 2001-05-08 |
| PRIOR APPLICATION NUMBER: USN 60/203,108 |
| NUMBER OF SEQ ID NOS: 3 |
| SOFTWARE: PatentIn version 3.0 |
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CF147821 AGENCOURT
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CF147822 AGENCOURT
                                                           October 1, 2004, 11:11:14 ; Search time 3517 Seconds (without alignments) 9985.193 Million cell updates/sec
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VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT ACCESSION REFERENCE AUTHORS

BX643713

BXFZp781C0629_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DKFZp781C0629_5', mRNA sequence. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

[(bases 1 to 839)
Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
EST (Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003) Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer
Research Center (DKEZ), Email S. Wiemann@dkfz- heidelberg.de,
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.

This clone (DKFzp781C0629) is available at the RZFD in Berlin. BX643713.1 GI:34478046 sapiens (human) Contact: MIPS Homo sapiens EST. Homo DEFINITION RESULT 1 BX643713

ALIGNMENTS

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  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                                                                                                                                                                                                                839;
             Charlottenburg, GERMANY; Email: Glone@rzpd.de
Location/Qualifiers
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                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                Score 438.6; DB 13;
Pred. No. 7.7e-100;
0; Mismatches 174;
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                                                            organism="Homo sapiens"
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al Similarity 75.9%;
570; Conservative (
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RESULT 2

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/tissue_type="mixed"
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Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                    Contact: Daniels S. Gerhard, Ph.D.
Contact: Daniels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llhl.gov
plate: IRBO2 row: b column: 07
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 704)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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.larity 77.0%; Pred. No. 9e-97;
Conservative 0; Mismatches 156;
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Location/Qualifiers
                CEL4/821
AGENCOURT 14740195 NIH MGC_145 H
MAGE:6971900 5', mRNA sequence.
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/clone="IMAGE:6971900"
                                                                                                                 CF147821.1 GI:33244089
                                                                                                                                                             Homo sapiens (human)
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/d_ne=IMAGE:6971899"
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/lab_host="MultoB"
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/lab_host="Wector: pcDNR3.1; Site_1: varies by clone; Site_2: varies by clone; ORFS were PCF=amplified and cloned into pcDNR3.1 by the GPRC Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/Khol-3', S'-EcoRV-XmnI/Khol-3', For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 732)

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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, WD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
CDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
                                              358 criccicerdediecericidaticcaridadenaceraridadenaceacearie
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone IMAGE:6971899 5', mRNA sequence.
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TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                    423 ACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGATGGTTCTTGGAAGAAGAGCAC 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                 483 GAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCCTCACCATTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             475 TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACATC
TTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 GCTGGCCTTCTTAGTGAATGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA----
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/mol_type="mRNA"
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/clone="urgpl-00001-d6"
/clone="lib="urgpl (14349)"
/note="Vector: pSPORT1; Rat GPCR library rearrayed internal pSPORT vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
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al Similarity 57.2%; Score 135.8; DB 14; Length
al Similarity 57.2%; Pred, No. 2.2e-23;
267; Conservative 0; Mismatches 197; Indels
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Plate: 00001 row: d column: 6.
Location/Qualifiers
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Rattus norvegicus
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
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Best Local S:
Matches 267
303
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TITLE
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KEYWORDS
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CC481311 684 bp DNA linear GSS 16-JUN-2003 CH240 309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 684)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B phage-resistant)"
/lab_host="DH10B pkgC Eyel"
/lone lib="MICHD KGC Eyel"
/note="Organ: eye; Vector: pCMV-SPORT6; Site I: NotI;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2:3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
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                                          Tissue Procurement:

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMM4564 row: f column: 24

High quality sequence stop: 707.
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Pred. No. 1.1e-21;
0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xenopus laevis"
/mol type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6949081"
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (XGC) library."
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Best Local Similarity 58.7%;
Matches 243; Conservative
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National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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Matches 329; Conservative
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

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LOCUS DEFINITION

RESULT 5 CD326085

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341

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Email: tropGeanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TEGG022i22.plkSp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CONSTRUCTED To primed from Sug of poly A+ RNA from egg.
ECORI.NotI cut cDNA was then ligated into pCS107 with EcoRI at the
Vector: pCS107; Site 1: ECORI, Site_2: NotI
Host: Escherichia_coli XL1-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 GGTTTGATTTCCATTCCTCTGTACATCCCTCACGTGTTGTTT----AACTGGAATTTTGGA 249
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.

(bases 1 to 643)

Croning, M. D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Unpublished (2003)

Unpublished (2003)

On Sep 15, 2002 this sequence version replaced gi:22868310.

Sanger Institute
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Pred. No. 4.4e-14;
0; Mismatches 180; Indels
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/db_xref="taxon:8364"
/clone="TEgg022i22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
British column: 10
Seg primer: T7
Class: BAC ends.
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Bovine BAC, End Sequences from Library CHORI-240, PLATES 294 to 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAATTATTTTTTTTTTTGGCTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTCC
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ
Tel: 604-877-6085
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AL848045.2 GI:38559584
EST.
Silurana tropicalis (western clawed frog)
Silurana tropicalis
                                                                                                                                                                                                                              Unpublished (2003)
Other GSSs: CH240 309C10.TARBAC13P2
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
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      AUTHORS
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BQ950659 1046 bp mRNA linear EST 21-AUG-2002 AGENCOURT 8863943 NIH_MGC_129 Mus musculus cDNA clone IMAGE:63119325', mRNA sequence.
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Nath-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
TITCITGGTAAATGGCCCCGAIGAITCTGGCTTCAGA-----TICITGGAAGAACAGCAC 482
                                                                                         298 critecierararesecerecearecidaerreseaenecrereregedesenerear 357
                                                                                                                               483 GAACACAAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCCACCATTACAAT 542
                                                                                                                                                                  ccccaaggccacricaracricaricaracracaacrigaracritaricarcaggcca 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13736 row: k column: 05
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Location/Qualifiers
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Best Local 9
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BQ950659
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                                                             BF567596
UI-R-BOO-agr-c-06-0-UI.rl UI-R-BOO Rattus norvegicus cDNA clone
UI-R-BOO-agr-c-06-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 cceaeeccricrecaaecrerescrescrestastataccracrestrescrescrestres 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATATTGTCCTCATTAGCTACGATCGATACCAGTCAGTTTCAAATGCTGTGTCTTATAG 368
                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                         1 (bases 1 to 499)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 3e-13;
0; Mismatches 190;
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97044477
                                                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                             BF567596.1 GI:11677326
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Best Local Similarity 54.5%;
Matches 238; Conservative (
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                                                                                                                                               VERSION
KEYWORDS
SOURCE
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                                RESULT 8
BF567596
LOCUS
DEFINITION
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/clone libe="CSEQRBN20"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: Not!; This normalized library was constructed from
Site_2: Not!; This normalized library was constructed from
I million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (Ks)+ vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
                                                                                                                                                                  1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BU468854 10-NOV-2002 154 bp mRNA linear EST 30-NOV-2002 603373878F1 CSEQREN20 Gallus gallus cDNA clone ChEST284119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 754)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                     1009 CCCAAATCGGTGTGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAAT 1068
528 TGCTGGGCCCCCTACACGCTGCTGATGATCATCCGCGCGCCTGCAGCGGGCAGGTGCGTGG 469
                                                                                                       468 ccGactac -- regraceacaraccricrescrererescreaereaereae
                                                                                                                                                                                                 412 CCCTTCCTGTACCCGCTGTGCCACAGCAGCCTTCCCGAGGGCTTTCTCCCAGAGGTCCTGTGT
                                                                                                                                                             1069 CCCTITCTGTACCCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                    1129 GTGACAAAGCAACCAGCGCTGTCACAGAACCAGTCAGTATCTTCTTGA 1176
                                                                                                                                                                                                                                                                                                                       352 ccchahagachgrcgcrrchgchrcghgrcghgrcgrchgrrhha 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="Layer and broiler"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Simon.Hubbard@umist.ac.uk.
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/clone="ChEST284119"
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1. .754
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/lab_host="DH10B"
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Gallus gallus
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis genome survey sequence T7 end of clone 206009 of library G from Tetraodon nigroviridis, genomic survey sequence
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                      GIGTCTTATAGGGCTCAACACACACGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTT 417
                                                                   608 dicricciacceseceaceagascacacacacacacaciericacaacaisarescacresis 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS; genome survey sequence.

Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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/clone lib="G"
/note="Genoscope sequence ID : C0AG206CB05LP1~end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                           418 TGGATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATT 466
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0; Mismatches 114; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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ilarity 59.0%; Pred. No. 3.5e-11;
Conservative 0; Mismatches 114;
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AL224547.1 GI:7883412
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Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
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Pred. No. 2.1e-09;

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55.3%;
                                      Matches 178; Conservative
              Best Local Similarity
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/clone lib="Meloidogyne hapla J2 pAMP1 v1"
/clone lib="Mector: pAMP1 (Gibco); Site 1: Noti; Site 2: Sall;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
McCarter at Washington University, St. Louis. The cDNA was
made by using pynabead oligo-dT priming (Dynal). DcR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
Williamson of the University of California at Davis
(vmwilliamson@ucdavis.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQB37058 505 bp mRNA linear EST 09-JAN-2003 rf37e04.yl Meloidogyne hapla J2 paMP1 vl Meloidogyne hapla cDNA 5' similar to TR:Q9XW31 Q9XW31 Y40H4A.l PROTEIN. [1] ;, mRNA sequence. BQ837058
                                                                                                                                                                             958 CCATACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCG 1017
                                                                                                                                                                                                                                                                         1018 GTGTGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTG 1077
                                           ij
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                           218 ccararacitriagraargarrarrcgiggagccrgcc---aaagrgaargrgccarrca 274
                                                                                                                                                                                                                                                                                                        158 GACAAGAATTGCAAAGTCACTTGCCATAATTGTGTGTGTCTTTGCCATTTGCTGGGCC 217
                                                                                                                                                                                                                                                                                                                                                                  335 TACCCTCTCTGTCATGATAAATTTCGAATGGCTTTTATGAAAAATTTATGTCCCAAGAA 393
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkey, Box 8501, St. Louis, MO 63108, USA
Fig. 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone will not be made available due to an unidentified
microbial contamination of the source material.
Seq primer: -40RP from Gibco
                                           3;
                                                                                         898 GGCAGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCAT
                                           Indels
. No. 2e-09;
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/mol type="mRNA"
/db_xref="taxon:6305"
/dev_stage="J2"
                                         0; Mismatches
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Location/Qualifiers
                     Pred.
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/lab_host="DH10B"
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                   Best Local Similarity 61.5
Matches 147; Conservative
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AUTHORS
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BQ837058
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DB 13; Length 505;

Score 80.4;

6.8%;

Query Match

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Exa: 402 762 4360
Exa: 102 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980994.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 25-APR-2001
                                                                                                                                                                                              141 crerrecrearcharcharnesechartricharnecharatricharatacesea 200
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.

(bases 1 to 258)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                              TGGCATTTTTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCT
                                                                                                                                21 TIGIAATTATIGGATTATITITICICATIAGCIACAACGATCGGGAATGCICTIGITAIGC
                                                                                                                                                                                                                                                                81 TITCIATITGIGITGATAAAAATTACAAATTAGCAATTATTITCITTTTAG
                                                                                                                                                                                                                                                                                                                                  173 CTATITICIGACTICCTCGTGGGTTTGATITICCATICCTC---IGTACATCCCTCACGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 IGITIAACIGGAATITIGGAAGIGGAATCIGCAIGITITIGGCICATIACIGACIAICITI
3;
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0; Mismatches 141; Indels
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/lab_host="DH10B"
/clone_lib="MARC_1BOV"
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/mol_type="mRNA"
/db_xref="taxon:9913"
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 96 row: K column: 4
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Bos taurus
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Similarity
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1 (bases I to 41).

1 (bases I to 41).

2 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Harvey, N., Schurk, R., Allen, M., Person, B., Swaller, T., McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington Univ. Nematode EST Project, 1999
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//note="Vector: pAMP1 (Gibco); Site 1: NoTi; Site 2: Sall;
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna)]. PCR based Synthesing a medified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. J2 were provided by Dr. Valerie
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/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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This clone will not be made available due to an unidentified
microbial contamination of the source material.
Seq primer: -40RP from Gibco.
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Pred. No. 2.1e-09;
0; Mismatches 94; Indels 0
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/organism="Meloidogyne hapla"
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/db_xref="taxon:6305"
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Matches 136; Conservative
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REFERENCE AUTHORS

COMMENT

FEATURES

RESULT 14

BQ836551

VERSION

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BJ122942 BJ122942 unpublished oligo-capped cDNA library, C. elegans L1 stage caenorhabditis elegans cDNA clone ykl293h04 5', mRNA sequence.
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and Sugano,S.
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Williamson of the University of California at Davis (vmwilliamson@ucdavis.edu)."
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                                                                                                Length 410;
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Pred. No. 3.1e-08;
                                                                                                                                             Indels
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Contact: Tadasu Shin-i
Centact For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                         6.7%; Score 78.8; DB 13;
55.0%; Pred. No. 5.1e-09;
iive 0; Mismatches 142;
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/dev_stage="L1"
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/clone="yk1293h04"
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/strain="N2"
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198 GGTGTCATATCAATACCCATGTTCACATACTACACATTCAAAATGGGATCTTGGA 257
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                               133 AACCTTAGACATCGAAGTAATTATTTTTTTTTTGGCTATTTCTGACTTCCTCGTG 192
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               Copyright
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em_htg_vrt:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1538 bp mRNA linear ROD 02-SEP-2001 H4 receptor mRNA, complete cds.

ALIGNMENTS

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AF358859
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1538)

Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.

Comparison of human, mouse, rat, and guinea pig histamine H4

receptor suggests substantial species variation

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CCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
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Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
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McPherson, J.D. and Waterston, R.H.
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 200346)
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Mus musculus (house mouse)
Mus musculus
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Submitted (25-AUG-2002)
Parkway, St. Louis, MO (
3 (bases 1 to 200346)
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// translation="MSENSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDR
// translation="MSENSTGILPPAAQVPLAFNWNFCSGICWFWLITDYLLCTASV
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
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Mus musculus chromosome UNK clone RP23-314021, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center, 4444 Forest Park 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park
                                                                                                                                                                                                                                                           Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vidaces I Co 2003-207, Wilson, R.K.
Direct Submission
Direct Colombiasion
Submitted (106-NOV-2003) Genome Sequencing Center, 4444 For Parkway, St. Louis, MO 63108, USA
On Nov 6, 2003 this sequence version replaced gi:22475584.
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us-10-626-445-5.olig.rge

m

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93120
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/db_xref="GI:15420537"
/translation="MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases I to 1593)
Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                 93239 TCCTTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGCAGTACGCAGAGCTTCTCAGA
                                                                                                                                                                                                                                                                                                                                             93179 GGCAGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93059 GIGIGGTACAGCATIGCCTICTGGCTGCAATGGTTCAATTCGTTTAATCCCTTTCTG
                          93299 AGCATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTAATCCCTTTCTG
                                                                                    AGCATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGT
                                                                                                                                                                                                                                          TCCTTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGA
                                                                                                                                                                                                                                                                                                                       898 GGCAGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1593)
Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus histamine H4 receptor mRNA, complete cds. AF358860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="G-protein-coupled receptor"
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/product="histamine H4 receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
36. .1211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                      Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer B1; 0% of reads
Chemistry: Dye-terminator B1; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199211 bases at least Q40
Consensus quality: 199515 bases at least Q20
Insert size: 199000; agarose-fp
Insert size: 199000; agarose-fp
Insert size: 199909; sum-of-contigs
Quality coverage: 13.37 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%; Score 819; DB 2; Length 200346; 100.0%; Pred. No. 0; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56: contig of 56 bp in length
156: gap of unknown length
17 1270: contig of 1114 bp in length
1 1370: gap of unknown length
1 85906: contig of 84536 bp in length
17 86006: gap of unknown length
17 200346: contig of 114340 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157. 1270
/note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig16"
86007. .200346
/note="assembly_name:Contig17"
------ Project Information
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                  Center project name: M BA0314021
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Muzny, D. Marte., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, E., Alsbrooks, S., Amin, A., Anguiano, D.,
Bandaranaike, D., Barber, M., Barnetead, M., Benahmed, F.,
Bandan, C., Blair, J., Blankenburg, K., Blyth, B., Brown, M.,
Bryant, M., Blair, J., Blankenburg, K., Blyth, B., Brown, M.,
Bryant, M., Endre, C., Barber, M., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen
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TNTEECEPGEVTEWYILAITAFLEFLLPVSLVVYFSVQIYWSLWKRGSILSRCPSHAGF
THSSRGTGHERRTGLACKTSLPGLKRABASHABESPRGKSSLLVSLETHWSGSIIAF
KVGSFCRSESPVLHQRELVEGRKLARASLAVLLARAICWAPVLETTURG
ERPKSIWYSIAFWLQWFNSLINPFLYPLCHRRPQKAFWKILCVTKQPAPSQTQSVSS
                                                                                                                                                                                                                                                                                                                                                                                          230 IGTTTAACTGGAATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                   265 TGTTTAACTGGAATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGATGTTTT 324
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                 5.7%; Score 67; DB 10; Length 1593;
100.0%; Pred. No. 4e-24;
tive 0; Mismatches 0; Indels
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HTG, HTGS PHASE1, HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 777030, USA
On Nov 15, 2002 this sequence version replaced gi:23812823.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Stefanle, M., Strong, R., Sutten, E., Sore, J., Tsylor, T., Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, C., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, C., Wang, C., Warren, J., Warl, X., White, F., Wang, C., Warish, S., Warren, R., Wari, X., White, F., Walliams, G., Willson, R., Wleczk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
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Consensus quality: 175902 bases at least Q40
Consensus quality: 179521 bases at least Q30
Consensus quality: 181489 bases at least Q30
Estimated insert size: 182948; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GUEK
Center clone name: CH230-397N16
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Rat Genome Sequencing Consortium.
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Worley, K.C.
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/product="histamine H4 receptor"
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Pred. No. 0.042;
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100.0%; Pred. No. v...
0; Mismatches
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Cavia porcellus
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101_.1270
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Matches 26; Conserv
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Kamohara,M., Saito,T., Ohishi,T., Soga,T., Hiyama,H., Matsushime,H.
and Furuichi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA cloning and characterization of porcine histamine H4 receptor Biochim. Biophys. Acta 1575 (1-3), 135-138 (2002) 22015261
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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ilarity 100.0%; Pred. No. 2.9e-24;
Conservative 0; Mismatches 0;
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Matsumoto, S., Oda, T. and Saito, Y.
Direct Submission
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54. .1236
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FPSTAVYKFAFWLQWFNSCVNPFLYPLCHKRPOKAFLKTFCLKKQSTLGHNRSSTTN
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GFLSHSDSLALQQREHIELFRARKLAKSLAILLAAFAICWAPYSLTTVIYSFFPERNL
TKSTWYHTAFWLQWFNSFVNPFLYPLCHKRFQKAFLKILPVRRQSTPPHNRSIST"
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Liu.C., Whison,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
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Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
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Cavia porcellus histamine H4 receptor mRNA, complete cds.
AF3588958
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                                                                                                                                                                                                                                                                                                                  2.4%; Score 28; DB 4; Length 1291;
100.0%; Pred. No. 0.0036;
ive 0; Mismatches 0; Indels
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/note="G-protein-coupled receptor"
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PAT 18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
1 (Dases 1 to 1173)
Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L., Umland, S.P. and Wang, S.
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                                                                                                        Query Match 1.9%; Score 22; DB 11; Length 849; Best Local Similarity 100.0%; Pred. No. 6.2; Matches 22; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:10090"
/map=". X 27-768 11720021-11719276"
/clone_lib="CZECHII/Ei"
<1. .>849
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100.0%; Pred. No. 6.1;
iive 0; Mismatches
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Pred. No. 6.1;
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Patent: US 6613533-A 1 02-SEP-2003;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 6204017.
AR142850
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/mol_type="genomic DNA"
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AR142850
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 849)
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.,
Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome
Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as STSs and 81,000 SNPs were annotated with alleles from C5/BL/6J and the Strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers
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                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
                                                                                                                                                             Raponi,M.
Methods for assessing and treating leukemia
Patent: WO 03038129-A 697 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    1.9%; Score 22; DB
100.0%; Pred. No. 6.8
ive 0; Mismatches
 Sequence 697 from Patent WO03038129
                                                                                                                                                                                                                                                                                                /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/strain="CZECHII/Ei"
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BV056167
BV056167.1 GI:31171962
                      AX775381
AX775381.1 GI:32486897
                                                                          Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 22; Conservative
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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JP 2001211889-A/1.
Homo sapiens (human)
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A61K37/02,C12N5/00
Novel polypeptide
           Homo sapiens (human)
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BD015847
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BD015847
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1.9%; Score 22; DB 6; Length 1173;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels
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G-protein coupled receptor-like polypeptide
Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
1. 1173
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100.0%; Pred. No. 6.1;
Ative 0; Mismatches
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Histanine receptor
Patent: WO 0125432-A 112-APR-2001;
SCHERING CORPORATION (US)
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AXI39113
AXI39113.1 GI:14274791
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Sequence 1 from Patent W00185786.
AX301763 GI:17382844
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DEFINITION
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AX301763
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PN JP 2001211889-A/1

PD 07-AUG2-2001

PF 27-CCT-2000 JP 2000329359

PR 29-CCT-1999 GB 9925641:4,20-APR-2000 GB 0009973:9 PI

BEAT PETER, MARK ANTONY OLAYLEE

PC C12115/09, A61R38/00, A61R39/395, A61R48/00, A61P1/04,

PC A61P11/00,

PC A61P11/06, A61P29/00, A61P31/00, A61P37/02, A61P37/08,

PC A61P11/06, A61P29/00, A61P31/10, A61P37/02, A61P37/08,

PC CO7K14/705, CO7K16/28, C12N1/15, C12N1/12, C12N5/10, C12N9/ PC
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1 (bases 1 to 1173)
Peter, B. and Olaylee, M.A.
Novel polypeptide
Patent: JP 2001211889-A 1 07-AUG-2001;
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Location/Qualifiers
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Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
Human histamine h 4? receptor
Patent: WO 0185786-A 1 15-NOV-2001;
American Home Products Corporation (US)
Location/Qualifiers
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PARTICION AND CONTROL MENNA LINEAR PRI 14-NOV-2000 DEFINITION Homo sepiens histamine H4 receptor mRNA, complete cds.

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Query Match 1.9%; Score 22; DB 9; Length 1173; Best Local Similarity 100.0%; Pred. No. 6.1; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps

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 Search completed: October 1, 2004, 17:38:46 Job time : 4885 secs

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^{5829.499} Million cell updates/sec US-10-626-445-5 Perfect score:

3373863 seqs, 2124099041 residues

Searched:

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Post-processing: Listing first 45 summaries

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Farnesyl
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ALIGNMENTS

Histamine H4 receptor; mouse; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss. BP. Mouse histamine H4 receptor cDNA. AAI70981 standard; cDNA; 1176 entry) (first 18-MAR-2002 AAI70981; RESULT 1 AAI 7098:

22-FEB-2001; 2001WO-US005914. WO200192485-A1 Mus musculus 06-DEC-2001.

(ORTH) ORTHO-MCNEIL PHARM INC Lovenberg T, Liu C; WPI; 2002-114339/15 P-PSDB; AAM50565.

31-MAY-2000; 2000US-0208260P.

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

Claim 4; Fig 5A; 92pp; English.

The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The cDNA was isolated from a mouse spleen cDNA library. It shows 72.8% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, ra and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host calls that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of

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AA166009 AAS98078

¹ atgtcggagtctaacagtac......accagtcagtatcttcttga 1176 Sequence:

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diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may buseful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                         Length 1176;
                                                                                                                         Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;
                                                                                                                                                                                      Indels
                                                                                                                                                         DB 6;
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                                                                                                                                                                       Pred. No. 0;
0; Mismatches
                                                                                                                                                         Score 1176;
                                                                                                                                                         100.0%;
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                                                                                                                                                                       Best Local Similarity 100.
Matches 1176; Conservative
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The present sequence is that of a cDNA clone encoding a rat histamine receptor of the H4 subtype. The CDNA was isolated from a rat spleen CDNA library. It shows 72.54 homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AA170980-83) and polypeptides (see AAA70986-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian pharmacology of known histamine ligands is demonstrated. Mammalian of histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying may be useful for diagnosing, treating or preventing asthma, allergy, useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin
                                                                                                                                                                                                                                    encoding
it is
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                          AGGAAGCTAGCCAGGTCACTGGCCATCTTTTGTTTTGCTGGCTCCA
                                                                                                        961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGCCCCCAAATCGGTG
                                                                                                                                          TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTTAAC
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AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA
                                                                     TACTGTCTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAAATCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian histamine H4 receptor proteins and polynucleotides the proteins, useful in gene therapy for treating diseases where beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                          1176
                                                                                                                                                                                                                                                                                        CCAGCGCTGTCACAGAACCAGTCAGTATCTTGA 1176
                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat histamine H4 receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAI70982 standard; cDNA; 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2001; 2001WO-US005914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus.
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                                                                                                                                                                                                         289
                                                                                                                                                                      230 TGTTTAACTGGAATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
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the proteins, useful in gene therapy for treating diseases where it is
beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                         230 TGTTTAACTGGAATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTT
dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histamine H4 receptor; mouse; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; PCR primer; RACE; ss.
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0
                                                                                           Length 1176;
                                                        Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;
                                                                            DB 6; Leus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30 BP; 8 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
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                                                                                         5.7%; Score 67; DB 100.0%; Pred. No. 9.2 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             AAI70992 standard; DNA; 30 BP.
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                                                                                                                                 67; Conservative
                                                                                                                                                                                                                                              290 TGTGCAC 296
                                                                                                                                                                                                                                                                                 290 TGTGCAC 296
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                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Length 30;

2.6%; Score 30; DB 6; I 100.0%; Pred. No. 0.00026;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperglycemia, constipation, arrhythmia, disorders of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                Histamine H4 receptor; mouse; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; PCR primer; RACE; ss.
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                                                                                                                                                                                                                                             Mouse histamine H4 receptor gene specific primer P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29 BP; 9 A; 10 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes mellitus, hyperglycemia, constipation, the neuroendocrine system, stress and spasticity
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Pred. No. 0.00081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 2.5%; Score 29; up Local Similarity 100.0%; Pred. No. 0.0
741 IGCAICICGICACICAGAAAGICCICGAAG 770
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                               1 TGCATCTCGTCACTCAGAAAGTCCTCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 48; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2000; 2000US-0208260P.
                                                                                                                                 AAI70991 standard; DNA; 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C;
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AAI70983

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New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farnesyl transferase inhibitor modulated leukemia associated gene #700.
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Pred. No. 0.8;
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diagnosis; gene therapy; PCR primer;
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100.0%; Pre-
                                                                                                                                                                                                                                                                                               (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system, stress and spasticity
                                                                                                                                                                                                22-FEB-2001; 2001WO-US005914.
                                                                                                                                                                                                                                              31-MAY-2000; 2000US-0208260P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-2002; 2002WO-US034784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-2001; 2001US-0338997P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE85481 standard; DNA; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-114339/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003038129-A2.
                                                                                                 WO200192485-A1
                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                Lovenberg T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
                                                                                                                                                  06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE85481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE85481
ID ADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a cDNA clone encoding guinea pig

histamine receptor of the H4 subtype. The cDNA was isolated from a bone

arrow cDNA library. It shows 75.6% homology to the human H4 receptor

coding region. The invention provides mammalian (human, mouse, rat and

coding region. The invention provides mammalian (human, mouse, rat and

coding region. The invention provides mammalian (human, wee ben

expressed in recombinant host cells that produce active recombinant

protein. The pharmacology of known histamine ligands is demonstrated.

Mammalian histamine H4 receptor may be used in gene therapy for the

creatment of diseases where it is beneficial to elevate mammalian

chistamine H4 receptor activity. Recombinant protein is useful for

dentifying wodulators of the mammalian histamine H4 receptor. Such

codulators may be useful for diagnosing, treating or preventing asthma,

allergy, inflammation, cardiovascular and cerebrovascular disorders, non-

insulin dependent diabetes mellitus, hyperglycemia, constipation,

arrhythmia, disorders of the neuroendocrine system, stress and spasticity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                             Histamine H4 receptor; guinea pig; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histamine H4 receptor, mouse, antiasthmatic, antiallergenic, antiinflammatory, cardiant, circulatory, antidiabetic, laxative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 1170; 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse histamine H4 receptor cDNA forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%; Score 26; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 TTTTGGCTCATTACTGACTATCTTTT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 TTTTGGCTCATTACTGACTATCTTTT 287
                                                                                               Guinea pig histamine H4 receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 6B; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI70993 standard; DNA; 39 BP.
                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2001, 2001WO-US005914.
                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2000; 2000US-0208260P.
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                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lovenberg T, Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114339/15.
P-PSDB; AAMS0567.
                                                                                                                                                                                                                                              Cavia porcellus.
                                                                                                                                                                                                                                                                                               WO200192485-A1.
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                                                18-MAR-2002
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Gaps

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0; Indels

Pred. No. 0.8 Mismatches

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Brown JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
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                                                                                                                                                                                                                                                                      methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient
                                                                                                                                                                                                                                                                                                corresponds to a gene whose expression may be
                                                                                                                                                                                           The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl) (1-methyl-1H-imidazo]-5-yl)methyl]-4-(3-chlorophenyl)-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmory disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; oardiovascular activity disorder; pain perception disorder; obesity; diabetes;
                                                                                                                        farnesyl
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                      Determining whether a patient will respond to treatment with a farr transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                           1.9%; Score 22; DB 9; Length 223; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DNA for potential G protein-coupled receptor #107.
                                                                                                                                                                                                                                                                                                                                    Sequence 223 BP; 57 A; 49 C; 43 G; 73 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                    Disclosure, SEQ ID NO 700; 346pp; English
                                               (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperlipidaemia; stroke; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                          197 TCTGTTCACAATTGTCCTTTCA 218
                                                                                                                                                                                                                                                                                                                                                                                                            966 TCTGTTCACAATTGTCCTTTCA 987
                                                                                                                                                                                                                                                                                                           modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS98150 standard; DNA; 540 BP
          30-OCT-2001; 2001US-0340938P. 30-OCT-2001; 2001US-0341012P.
                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2001; 2001WO-US015332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2000; 2000US-0203217P.
18-MAY-2000; 2000US-0205945P.
30-OCT-2001; 2001US-0340081P.
                                                                                                                                                                                                                                                                                              respond. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                               WPI; 2003-513497/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001
                                                                        Raponi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS98150;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
AAS98150/c
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GGPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antiesnse probes), a host call comprising an expression vector comprising the GPCR sequence.

CC antibodies raised against the polypeptides are useful for cell comprising modulator compounds which function as modulators, activators, identifying modulator compounds which function as modulators, activators, crepressors, against the polypeptides and mucleic acid probes as including the GAL4 polypeptide. The antibodies and nucleic acid probes as confined above can be used to discose and nucleic acid probes as including the GAL4 polypeptide. The antibodies and nucleic acids and are used to discose a variety of disease.

CC discorders in which GPCRs are involved e.g., Alzheimer's disease or discorders in which GPCRs are involved e.g., Alzheimer's disease.

CC discorders in which GPCRs are involved e.g., Alzheimer's disease.

CC arctinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, depression, epilepsy, macular degeneration, lymphoma, melanoma, multiple sclerosis, rheumatoid costeoarthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disease, psoriasis, heumanosis consecues, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidademia and stroke. The their when the present sequence is a novel GPCR polynucleotide of the their work of the present sequence is a novel GPCR polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; H4; histamine receptor; inflammatory bowel disease; psoriasis; atopic dermatitis; stroke; myocardial infarction; migraine; allergy; chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy; rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective; asthma; receptor; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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100.0%; Pred. No. 2.5;
tive 0; Mismatches 0; Indels
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    Fabre-Suver C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human H4b protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human H4 receptor splice variant (H4b) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2, Page 106; 144pp, English
    Burmer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              966 ICTGTTCACAATTGTCCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD55123 standard; DNA; 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-AUG-2003 (first entry)
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hes 22; Conservative
Miller M,
                                                                                             WPI; 2002-066595/09
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Novel splice variants of human H4 histamine receptor, H4b and H4c, useful for identifying agonists or antagonists of the receptor which are useful for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, H4; histamine receptor; inflammatory bowel disease; psoriasis; atopic dermatitis; stroke; myocardial infarction; migraine; allergy; chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy; rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective; asthma; receptor; gene; ds.
                                                                                                                                                                                                                                                                                                                The invention relates to splice variants of human H4 histamine receptor, H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, mycoardial infarction, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, or psoriasis. The present sequence is human H4c DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9%; Score 22; DB 8; Length 1166;
100.0%; Pred. No. 2.5;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1166 BP; 294 A; 246 C; 218 G; 408 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Human H4 protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                               Claim 17; Page 48-49; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       915 rcrerrcacharrercerrrca 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human H4 receptor wild-type DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               966 TCTGTTCACAATTGTCCTTTCA
13-NOV-2001; 2001US-0332697P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD55126 standard; DNA; 1170
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13-NOV-2001; 2001US-0332697P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.3
Best Local Similarity 100.
Matches 22; Conservative
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                                                                                    Yates SL;
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                                          (MERI ) MERCK & CO INC
                                                                                                                              2003-290186/28.
                                                                                                                                                  P-PSDB; AAE36415.
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                                                                                    Gallagher MJ,
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                                                                                                                                                                                                                                                                                                                                                               Novel splice variants of human H4 histamine receptor, H4b and H4c, useful for identifying agonists or antagonists of the receptor which are useful for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; H4; histamine receptor; inflammatory bowel disease; psoriasis; atopic dermatitis; stroke; myocardial infarction; migraine; allergy; chronic obstructive pulmanary disease; COPD; cerebroprotective; therapy; rheumatoid arthritis; multiple solerosis; inflammation; neuroprotective; asthma; receptor; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to splice variants of human H4 histamine receptor, H4b and H4c. The invention is useful for identifying an agonist, antagonist of amammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chromic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, or psoriasis. The present sequence is human H4b DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1103 BP; 275 A; 226 C; 217 G; 385 T; 0 U; 0 Other;
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100.0%; Pred. No. 2...
... 0; Mismatches
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55. .1128
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13-NOV-2001; 2001US-0332697P.
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                                                                                                          30-AUG-2002; 2002WO-US027891
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                           Yates SL;
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                                                                                                                                                                                                                                                         Gallagher MJ,
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RESULT 10 AAD55

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98US-0109213P
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Best Local Similarity
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29-SEP-1999;
29-SEP-1999;
01-0CT-1999;
01-0CT-1999;
01-0CT-1999;
01-0CT-1999;
12-0CT-1999;
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                                                                                                                                                                                                                                           Behan DP,
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                                                    Novel splice variants of human H4 histamine receptor, H4b and H4c, useful for identifying agonists or antagonists of the receptor which are useful for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical; mutant;
                                                                                                                                                                   The invention relates to splice variants of human H4 histamine receptor,
                                                                                                                                                                                H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migratine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, or psoriasis. The present sequence is human H4 receptor DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13
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0
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                                                                                                                                                                                                                                                                                                                                  Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;
                                                                                                                              Disclosure; Page 56-58; 31pp; English.
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98US-0109213P.
98US-0109213P.
99US-0123944P.
99US-0123944F.
99US-0123946P.
99US-0123946P.
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99US-0133946P.
99US-013643PP.
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 2003-290186/28
                 P-PSDB; AAE36417
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28-MAY-1999
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The present invention describes transmembrane receptors, preferably human grotein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-endogenous, human G protein-coupled receptors for scr
inverse or partial agonists useful as therapeutic agents.
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Liaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                     990S-015663F.
990S-0157280P.
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cocation/Qualifiers

.1173 *tag=

/product= "PFI-013"

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New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
osteopathic, neuroprotective, nootropic; dermatological; gynecological; signal transduction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 43; 66pp; English.
                                                                                                                                                                              24-OCT-2000; 2000EP-00309364.
                                                                                                                                                                                                       29-OCT-1999; 99GB-00025641.
20-APR-2000; 2000GB-00009973.
                                                                                                                                                                                                                                                                                  Peter B, O'reilly MA;
                                                                                                                                                                                                                                                                                                          WPI; 2001-309854/33.
P-PSDB; AAB62445.
                                                                                                                                                                                                                                          (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a cDNA encoding hRUP7, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned BY RT-FCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic; antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
                                                                                                                                                                                                                                                                                                                                                                                     Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GPCR-like polypeptide, PFI-013 encoding cDNA.
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Best Local Similarity 100.
Matches 22; Conservative
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This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor (GPCR) like polypeptide, designated PFI-013. The PFI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of PFI-013 are useful in the manufacture of a medicament for treating of PFI-013 are useful in the manufacture of a medicament for treating allergic disorder, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstitial and other pulmonary disease, including chronic obstructive pulmonary disease (COPD), infectious, inflammatory disease, such as inflammatory bowel diseases (COPD), infectious, inflammatory disease, reproduction and sexual diseases, psychotherapeutics, urogenital disease, reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, photoageing, skin pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The PPI-013 protein and nucleic acid are useful in the diagnosis and treatment of the above conditions and also for screening drug candidates for the treatment of diseases associated with
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Human G protein-coupled receptor, 7TM receptor; histamine H3 receptor homologue; infection; viral; bacterial; fungal; bistamine H3 receptor homologue; infection; viral; bacterial; fungal; protozoan; H1V-1; H1V-2; pain; cancer; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delizium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; falles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery;

Homo sapiens.

Key Location/Qualifiers
1. .1173
/*tag= a
/product= "Human AXOR35"
/note= "G protein-coupled receptor"

WO200133221-A1.

10-MAY-2001.

26-OCT-2000; 2000WO-US029461.

02-NOV-1999; 99US-00431898. 03-FEB-2000; 2000US-00497790. (SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC.

Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Michalovich D, Morrow DM, Zhu Y;

Li X;

WPI; 2001-316464/33.

P-PSDB; AAB73622.

Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.

Claim 2; Page 49-50; 54pp; English.

The invention relates to the human G protein-coupled receptor AXOR35

(AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments

CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative

CT transmembrane domains and is involved in signal transduction. AXOR35 has

homology and structural similarity with G protein-coupled receptors such

as the human histamine H3 receptor. The invention also relates to

expression vectors and host cells comprising AXOR35 DNA, to recombinant

expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins

concleotides may be used to treat a wide variety of disorders

including bacterial, fungal, protozoal and viral infections, particularly

HIV-1 or HIV-2 infections; palm; cancers; benign prostatic hypertrophy;

diabetes; obesity; anorexia; bullimia; osteoporosis; asthma; allergies;

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credicate are also and antibodies are also

credicated and neurologies, macrophages, eosinophils or neutrophils in

asthmatic lung. AXOR35 proteins, nucleotides are also

useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via the detection of mutations in the corresponding gene. AXOR35 proteins are CC also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nucleotides are CC also useful as diagnostic reagents, in chromosome localisation and tissue cycression studies, and for producing transgenic animals useful in drug discovery. AXOR35-specific antibodies are useful for purifying the AXOR35 protein or fragments thereof, and are also useful for treating conditions associated with the expression of the AXOR35 protein. The present CC sequence represents cDNA encoding human AXOR35

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Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-489-039A-7167

US-09-254-465A-7

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US-09-021-465A-7

US-09-021-465A-7

US-09-016-434-1103

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APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Haz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Willard, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTYON: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
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APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Morse, Kelley L.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CNO1069
CURRENT FILLING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             987
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                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09414010
, Patent No. 6204017
, GENERAL INFORMATION:
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Patent No. 6613533
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Best Local Similarity 100.0%; Pi
Matches 22; Conservative 0;
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   1590
1620
1744
2088
2088
2176
2181
2565
2861
4747
4747
6042
6042
6172
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Sequence 11, Application US/08466103A Patent No. 5856124
                 939 TITIGCCATTIGCTGGGCTCC 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0078(
TELECOMMUNICATION INPORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence LOCATION: JOCATION: 33...1082
OTHER INFORMATION:
US-08-466-103A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                           US-08-466-103A-11
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Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                  1.9%; Score 22; DB 4; Length 1173; 100.0%; Pred. No. 0.19; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Reppert, Steven M.
APPLICANT: BLisaw, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATE: US/08/466,103A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00786/250002
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CLASSIFICATION: 435
PRIOR APPLICATION DATE: 08/319,887
RILING DATE: 07-0CT-1994
PRIOR APPLICATION DATE: 08/261,857
FILING DATE: 17-UN-1994
ATTORNEY/AGENT INFORMATION: NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REPREBNENCE/DOCKET NUMBER: 00786/2: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 867 base pairs TYPE: nucleic acid STRANDENBESS: double
                                                                                                                                                                                                                                                                         966 TCTGTTCACAATTGTCCTTTCA 987
                                                                                                                                                                                                                                                                                                      960 TCTGTTCACAATTGTCCTTTCA 981
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US-08-466-103A-5
; Sequence 5, Application US/08466103A
; Patent No. 5856124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 1...864
CTHER INFORMATION:
US-08-466-103A-5
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1173
                                                                                                                                                                                                                                22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                            Similarity
                                                                                                                                  ; ORGANISM: m
US-09-812-216-1
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Best Local S
Matches 22
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                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Ediswa, Takashi
TITLE OF INVENTION: HIGH-APFINITY MELATONIN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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ZIP: 02110-2804

COMPUTER READMABLE DISKETCE

MEDLIUM TYPE: DISKETCE

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

COMPUTER: TABLES OF WINDOWS SOFTWARE:

SOFTWARE: FASTER: WINDOWS VERSION 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,103A

FILING DATE: 07-0CT-1994

PRIOR APPLICATION NUMBER: 08/319,887

FILING DATE: 07-0CT-1994

PRIOR APPLICATION NUMBER: 08/319,887

FILING DATE: 17-UNN-1995

WINDOWS VARIANCE OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER OF COMPANIER
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US-09-016-434-1435
Sequence 1435, Application US/09016434
Patent No. 650038
GENERAL INFORMATION:
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US-09-635-872A-16/c; Sequence 16, Application US/09635872A; Patent No. 6534300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence
LOCATION: 49...1146
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 20; Conservative
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Best Local Similarity
Matches 19; Conserv
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALIO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
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Federat No. 5856124
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: RCEPTORS AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FLING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ZEller, March J.
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 9A-0002 US
TELECOMMUNICATION INFORMATION:
TELEPROME (650) 845-4166
INPORMATION FOR SEQ ID NO: 1435:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               940 TTTGCCATTTGCTGGGCTCC 959
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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02110-2804
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US-09-016-434-1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 F
CITY: Boston
                                                                                                                                                                                                              94304
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-466-103A-3
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Matches
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US-09-134-000C-1014/c

US-09-134-000C-1014/c

Sequence 1014, Application US/09134000C

Sequence 1014, Application US/09134000C

Sequence 1014, Application US/09134000C

GENERAL INFORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: UNCRENCE ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: UNCRENCE OF 13796-032

CURRENT FILING DATE: 1998-08-13

FRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 1014

LINGTH: 453
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00.0%; Pred. No. 2.1;
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Conservative 0; Mismatches
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,103A
FILING DATE: 06-UNN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRIOR APPLICATION NUMBER: 08/261,857
FILING DATE: 17-UNN-1994
ATTORNEY APPLICATION NUMBER: 08/261,857
FILING DATE: 17-UNN-1994
ATTORNEY AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/2500f
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: 617/542-5070
TELEPAN: 617/542-5070
TELEPAN: 1149 base pairs
LENGTH: 1149 base pairs
TENGRATION FOR SEQ ID NO: 3:
FENTANDEDNESS: double
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Gaps

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Sequence 16, Application US/09986552

Patent No. 6670165

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
FILE REFERENCE: 215089US77DIV US/09/986,552
CURRENT FILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN UNMER: 09/635,831
PRIOR FILING DATE: 1999-09-14
SEQ ID NO 16
SEQ ID NO 16
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09128155
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT PILING DATE: 1998-08-03
; EARLIER PILING DATE: 1998-06-04
; EARLIER PILING DATE: 1997-08-04
; MUMBER OF SEQ ID NOS: 18
; SOTTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
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100.0%; Pred. No. 8.3;
tive 0; Mismatches 0; Indels 0;
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  Length 5229;
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                                                 Indels
       DB 4;
7.3;
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    Query Match 1.6%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 7.3 Matches 19; Conservative 0; Mismatches
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                                                                                                 1022 GGTACAGCATTGCCTTCTG 1040
                                                                                                                                           2576 égracadearrecerrere 2558
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Best Local Similarity 100.
Matches 19; Conservative
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ORGANISM: Mus musculus
US-09-986-552-16
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US-09-986-552-16/c
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              APPLICANT: CANFIELD, WILLIAM
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
TITLE OF INVENTION: 1950-00-08
CURRENT APPLICATION NUMBER: 00/053,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CANFIELD, WILLIAM M
APPLICANT: CANFIELD, WILLIAM M
APPLICANT: CANFIELD, WILLIAM M
APPLICANT: CANFIELD, WILLIAM M
TITLE OF INVENTION: GLCNAC PHOSPHOTRANSFERASE OF THE LYSOSOMAL TARGETING PATHWAY
FILE REFERENCE: 210119USOCCONT
CURRENT APPLICATION NUMBER: US/09/636,060C
CURRENT FILING DATE: 2000-08-10
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFFWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 5229
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US-09-636-077A-16/C
; Sequence 16, Application US/09636077A
; Patent No. 6537785
; GRNERAL INFORMATION:
; APPLICANT: CANFIELD.
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION WIMBER: US/09/636,077A
; CURRENT APPLICATION NUMBER: 60/153,831
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR APPLICATION NUMBER: 60/153,831
; RIGHER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; TENGRE OF SEQ ID NOS: 52
; SEQ ID NO 16
; TENGRE OF SEQ ID NOS: 52
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100.0%; Pred. No. 7.3;
iive 0; Mismatches 0; Indels
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7.3;
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US-03-636-06C-16/c
Sequence 16, Application US/09636060C
; Patent No. 6642038
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CORGANISM: Mus musculus
US-09-635-872A-16
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
GENERAL INFORMATION:
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APPLICANT: Sika-aho, Matti
APPLICANT: Sika-aho, Matti
APPLICANT: Sika-aho, Matti
APPLICANT: Vikari, Liisa
APPLICANT: Vikari, Liisa
APPLICANT: Vikari, Liisa
APPLICANT: Saloheimo, Anu
APPLICANT: Saloheimo, Anu
APPLICANT: Marjatta, Ranua
TITLE OF INVENTION: Methods for isolating the genes, and methods for bleaching
TITLE OF INVENTION: lignocallulosic pulps
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch and Birch
STREET: PO BOX 747
CITY: Falls Church
STATE: VA
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1.5%; Score 18; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels
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ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: FORM:

MEDIUM TYPE: FORM:

MEDIUM TYPE: TOPOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,020

FILING DATE: 13-ANG-1997

CLASSIFICATION NUMBER: US 08/341,568

PILING DATE: 22-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: MUTDRY Jr. Gerald M

REGISTRATION NUMBER: 365-262P

TELECOMMUNICATION INFORMATION:

NAME: MUTDRY Jr. Gerald M

REGISTRATION NUMBER: 365-262P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-911-020-1
; Sequence 1, Application US/08911020
; Patent No. 5854047
                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: CDNA

CORGINAL SOURCE:

ORGANISM: Trichoderma reesei

STRAIN: QM9414

US-08-341-568-1
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8050
                                                                         LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                            SEQUENCE CHARACTERISTICS:
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-911-020-1
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Patent No. 5661021

Patent No. 5661021

APPLICANT: Buchert, Johanna
APPLICANT: Sika-aho, Matti
APPLICANT: Sika-aho, Matti
APPLICANT: Saloheimo, Anu
APPLICANT: Penttila, Marja
APPLICANT: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching lig
TITLE OF INVENTION: pulps
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 9
ADDRESPONDENCES:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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CUNTRY: US
COUNTRY: US
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REFERENCE/DOCKET NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 22; Matches 18; Conservative 0; Mismatches
135343 CCAGGTCACTGGCCATCCT 135325
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ORGANISM: Homo sapiens
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US-08-341-568-1
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Query Match 1.5%; Score 18; DB 2; Length 536; Best Local Similarity 100.0%; Pred. No. 22; Matches 18; Conservative 0; Mismatches 0; Indels
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Search completed: October 1, 2004, 18:39:40 Job time : 113 secs

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Sequence 697, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 13, Appl
Sequence 14, Appli
Sequence 26, Appli
Sequence 11, Appli
Sequence 11, Appli
                                                                                                           October 1, 2004, 17:38:54 ; Search time 660 Seconds (without alignments) 9033.046 Million cell updates/sec
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"Cgn2_6/ptodata1/pubpna/PCT_NEW_PUB.seq:*
"Cgn2_6/ptodata1/pubpna/PCT_NEW_PUB.seq:*
"Cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seq:*
"Cgn2_6/ptodata1/pubpna/USO7_NEW_PUB.seq:*
"Cgn2_6/ptodata1/pubpna/USO8_NEW_PUB.seq:*
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"Cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
"Cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
"Cgn2_6/ptodata1/pubpna/USO9_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-875-076-13

US-10-052-193-1

US-10-290-078-26

US-10-290-078-26

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                                                                                                                                                                                                                                                                                                                                       3340653 seqs, 2534783454 residues
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US-09-910-411-1
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Sequence 13, Appl Sequence 25, Appl Sequence 1, Appli Sequence 1, Appli Sequence 274218, Sequence 274218, Sequence 274218, Sequence 275, Appl Sequence 275, Appl Sequence 1185, Appl Sequence 1185, Appl Sequence 1185, Appl Sequence 263186, Sequence 263186, Sequence 263186, Sequence 263186, Sequence 253125, Sequence 253125, Sequence 253125, Sequence 253125, Sequence 1163, Appl Sequence 253125, Sequence 253125,	equence 3795 equence 3795 quence 21, A equence 2070
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ALIGNMENTS

US-10-283-975A-697

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TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
FILLE REPERENCE: CDS 293 FCT
CURRENT APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
PRIOR FILING DATE: 2001-10-30
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Sequence 697, Application US/10283975A Publication No. US20040110792A1 GENERAL INFORMATION:
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LOCATION: (1).7(223)
OTHER INFORMATION: N=any base
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Matches 22; Conservative
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100.0%; Pred. No. 0.93;
tive 0; Mismatches 0; Indels
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1.9%; Score 22; DB 9;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches
                                             APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Honomas M.
APPLICANT: Monsen, Frederick J. Jr.
APPLICANT: Morse, Kalley L.
APPLICANT: Unland, Shelby P.
APPLICANT: Unland, Shelby P.
APPLICANT: Unland, Suke
TILE REFERENCE: CN01069
CURRENT APPLICATION WUMBER: US/09/812,216
CURRENT APPLICATION NUMBER: 2001-03-19
PRIOR FILING DATE: 1999-10-07
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1173
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Sequence 1, Application US/09812216 Patent No. US20020098539A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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US-09-910-411-1
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US-09-910-411-1
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1.9%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 0.9
Matches 22; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
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PRIOR PLING DATE: 1999-03-12
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PRIOR PLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR PELING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
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PRIOR PLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/151,114
PRIOR PLING DATE: 1999-05-28
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; ORGANISM: Homo sapiens
US-09-876-252-13
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LENGTH: 1173
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Sequence 13, Application US/09876252

Publication No. US20030018182A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Lowitz, Kevin P.

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APPLICANT: Lowitz, Kevin P.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Lowitz, Kevin P.

FILE REFERENCE: ARNO-0034

CURRENT FILING DATE: 1999-10-12

PRIOR APPLICANTON NUMBER: 60/110, 416

PRIOR APPLICANTON NUMBER: 60/120, 416

PRIOR APPLICANTON NUMBER: 60/120, 416

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

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                           PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-09-29
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PRIOR FILING DATE: 1999-10-01
PRIOR PELICATION NUMBER: 60/157,291
PRIOR PELICATION NUMBER: 60/157,291
PRIOR PELING DATE: 1999-10-01
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FILING DATE: 1998-11-20
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FILING DATE: 1999-03-12
       FILING DATE: 1999-05-28
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; ORGANISM: Homo sapiens
US-09-875-076-13
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PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-38
NUMBER OF SEQ ID NOS: 74
SOUTWARE: PATENTIN Ver. 2.1
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1.9%; Score 22; DB 15; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: PFizer Inc.
APPLICANT: Peter, Beate
APPLICANT: Peter, Beate
TITLE OF INVENTION: NOVEL POLYPEPTIDE
FILE REFERENCE: PC10373B
CURRENT APPLICATION NUMBER: US/10/354,769
CURRENT FILING DATE: 2003-01-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1900-06-14
SERIOR FILING DATE: 1900-06-14
SERIOR FILING DATE: 1900-06-14
SERIOR FILING DATE: 1900-06-16
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10354769; Publication No. US20030149242A1; GENERAL INFORMATION:
FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-10-272-983-13
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Publicance 26, Application US/20030124596A1
Publicance 26, Application No. US20030124596A1
GENERAL INFORMATION:
APPLICANT: Carroll, Joseph A.
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE REPERENCE: MPIZO01-288PP(M)
TITLE REPERENCE: MPIZO01-288PP(M)
CURRENT APPLICATION NUMBER: US/110/290,078
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 265
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Sequence 13, Application US/10272983
; bublication No. US20030148450A1
; GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOOSO
; CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR APPLICATION NUMBER: 60/109,213
PRIOR PILING DATE: 1998-11-20
; PRIOR PILING DATE: 1998-11-20
; PRIOR PLING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR APPLICATION NUMBER: 60/121,851
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1.9%; Score 22; DB 14; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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  PRIOR APPLICATION NUMBER: 0101223.6
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10
SSCTWARE: Patentin Ver. 2.1
SSQ ID NO 1
LENGTH: 1173
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Best Local Similarity 100.0
                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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US-10-290-078-26
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ORGANISM: Homo Sapien
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Sequence 13, Application US/10417820A

Publication No. US20030229216A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Constitution Protein Coupled

TITLE OF INVENTION UNMERR: 09/416, 760

PRIOR APPLICATION NUMBER: 09/170, 496

PRIOR FILING DATE: 1998-10-13

PRIOR PELING DATE: 1998-11-27

PRIOR PELING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR PRIOR FILING DATE: 1998-11-20
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SECTIVARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
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APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
ITILE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOOSO
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CURRENT PELLING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: US/09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1998-11-20

PRIOR FILING DATE: 1998-11-20

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,557

PRIOR APPLICATION NUMBER: 60/136,557

PRIOR APPLICATION NUMBER: 60/136,557

PRIOR FILING DATE: 1999-05-28
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APPLICATION NUMBER: 60/123,944
FILING DATE: 1999-03-12
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; ORGANISM: Homo sapiens
US-10-393-807-13
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USS-10-782-596-13
USS-10-782-596-13
Sequence 13, Application US/10782596
Publication No. US20040137509A1
Sequence 13, Manual No. US20040137509A1
SERENAL INFORMATION:
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Liam Orphan G Protein Coupled Receptors TILLE OF INVENTION NUMBER: US/10/782,596
CURRENT FILING DATE: 2004-02-19
FRIOR APPLICATION NUMBER: 09/417,044
FRIOR PILING DATE: 1999-02-16
FRIOR PELING DATE: 1999-02-16
FRIOR APPLICATION NUMBER: 60/123,946
FRIOR APPLICATION NUMBER: 60/123,946
FRIOR APPLICATION NUMBER: 60/123,946
FRIOR APPLICATION NUMBER: 60/136,436
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FRIOR PILING DATE: 1999-05-28
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FRIOR APPLICATION NUMBER: 60/136,57
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100.0%; Pred. No. 0.93;
tive 0; Mismatches 0; Indels (
Query Match 1.9%; Score 22; DB 17; Length 1173; Best Local Similarity 100.0%; Pred. No. 0.93; Matches 22; Conservative 0; Mismatches 0; Indels
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Fublication No. US20040138234A1
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TITLE OF INVENTION:
FILE REFERENCE: PC10663A
CURRENT FILING DATE: 2003-12-16
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PRIOR APPLICATION NUMBER: 01223.6
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ 1D NOS: 10
SOFTWARE: PatentIn Ver: 2.1
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CRGANISM: Homo sapiens
US-10-737-619-1
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US-10-737-619-1
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CE700949 tigr-gss-A0390595 cITBI-EI-CE849215 tigr-gss-BZ227627 CH230-400 AY405331 ben capi AY405331 Pen trogl BG563625 602582370 CF661120 CcLiloa3 AA250969 zs07011.s

CB981626 CABTOONS
D70276 CELK101E1F
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CE642921 tigr-gss-AZ150613 SP 0045 B
AZ150613 SP 0045 B
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BF056033 7K07E09.x

Word size :

Searched:

Sequence:

Database :

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No.

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BH987629 oei37g11. CC752731 ZMMBBD013 CF538979 UI-M-GIO-

AZ381267 1M0137B15 CA375189 649814 NC CF147821 AGENCOURT

CB349043 CAB2SG000 AU217737 AU217737 CC960774 BOICC61TR

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Run on:

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CG392906 997 bp DNA linear GSS 22-SEP-2003 ZMMBBC0004Allf ZMMBBC (ECORI) Zea mays subsp. mays genomic clone ZMMBBC0004All 5', genomic survey sequence.
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Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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Zea mays subsp. mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae; Zea.
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
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190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 32 445 3801
Fax: 732 445 5735
Email: bhartigwaksman.rutgers.edu
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           AQ390595
AQ390595
AZ405331
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KEYWORDS
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COMMENT
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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CC226484 1051 bp DNA linear GSS 12-MAY-2003 CH261-69015 RM1.1 CH261 Gallus gallus genomic clone CH261-69015, genomic survey sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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100.0%; Pred. No. 3.1;
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Kremitzki, C., Higginbotham, J., Wylie, K., Carte Warren, W., Graves, T., Mardis, E. and Wilson, R. Gallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
                                                               'organism="Zea mays subsp. mays"
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Mashington University School of Medicine
Email: submissions@watson.wustl.edu
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/strain="Red Jungle Fowl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
                                                                               /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 19
High quality sequence stop: 360.
Location/Qualifiers
High quality sequence start: 97.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CH261-69015"
                                                                                                                                                                                                                                                                                                                                                                                 57 ATTITIAATGICITCATTIGCCT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC226484.1 GI:30553147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (chicken)
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KEYWORDS
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849 AATTATTTTTTTTGGC 827

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. S. I (bases 1 to 274)

RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Iaawa, M., Endo, T., Pukuda, S., Fukunishi, Y., Haza, A., Hayatsu, N., Ianawa, M., Kadota, K., Kagwa, I., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagwa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shipata, Y., Shinagawa, A., Shiraki, T., Tomanga, M., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshida, K., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hyashizaki, Y.
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RIKEN Mouse BSTS (Konno, H., et al.)

LUDUDISHED (2000)

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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/
URL:http://genome-gsc.riken.go.jp/
URL:http://genome-gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoachivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,X., Izawa,M., Kawai,J., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                               BB418962 RIXEN full-length enriched, 12 days embryo spinal cord Mus musculus cDNA clone C53004915 3' similar to AF117947 Homo sapiens PDZ domain-containing guanine nucleotide exchange factor I mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inche="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RIKEN full-length enriched, 12 days embryo spinal_cord"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="spinal cord"
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="C530014D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .274
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                                                                                                                                                                    mRNA sequence.
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JOURNAL
COMMENT
RESULT 3
BB418962
                                                                                                                                                                                                                                                  ACCESSION
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KEYWORDS
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ORIGIN

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: thol(@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
                                                prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' ASAGARAGATTCHCGAGTTATTAATAATTAATCCCCCCCCCCCC 3']. CDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
/cell_type="Blood"
/clone lib="CHORI-240"
/note="Vector: pTARBACL3; Site 1: MboI; Site 2: MboI;
/Hereford bull il Domino 99375; CHORI-240 Bovine BAC
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6 Tel: 604-877-6085
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                                                                                                                                                                                                                                                                                                             Query Match 1.9%; Score 22; DB 10; Length 274; Best Local Similarity 100.0%; Pred. No. 8.8; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Other GSSs: CH240_380N19.TARBAC13P2
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="breed: Hereford"
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                                                                                                                                                                                                                                                                                                                                                                                                                                150 TAATTATTTTTTTTG 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC584203.1 GI:31934631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 604-877-6276
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Bos taurus
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CC584203/c
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KEYWORDS
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602 bp DNA linear GSS 06-MAR-1999
CITBI-E1-2544B13.TR CITBI-E1 Homo saplens genomic clone 2544B13,
genomic survey sequence.
                                                                                                                                                                                                                          131 bp DNA linear GSS 29-SEP-2003 tigr-gss-dog-17000368904282 Dog Library Canis familiaris genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14512627
Contact: Kirkness BF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 331)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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/clone lib="Dog Library"
/note="Site l: BstXI; Libraries were prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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library (Male) produced by Pieter de Jong'
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                                                 DB 29;
9.9;
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/mol_type="genomic DNA"
/strain="Standard Poodle"
                                               1.9%; Score 22; DB ilarity 100.0%; Pred. No. 9.9 Conservative 0; Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                    370 GCTCAACACTGGCATCATGA 391
                                                                                                                                        635 GCTCAACACACTGGCATCATGA 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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Canis familiaris
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                                      Query Match
Best Local Similarity
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hes 21; Conserv
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LOCUS
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Shao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Uppublished (1997)
Other Gass: CITBLEL-2544B13.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Gail: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: MJ3 Reverse
Class: BAC ends.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
I (bases 1 to 722)
Kirkness E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="sperm"
/clone_tib="CirBl-E1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tigr-gss-dog-17000332984147 Dog Library Canis familiaris genomic, genomic survey sequence.
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/mol_type="genomic DNA"
/strain="Standard Poodle"
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1.8%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Location/Qualifiers
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Fax: 301-838-0208
Email: ekirknes@tigr.org
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E 1 (Dases 1 to 861)

Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,

Shatstsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,

Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 MboI segment

Unpublished (1999)

Other_GSs: CH230-40017.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 400 row: N column: 17
Class: BAC ends.
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CH230-400N17.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-400N17, genomic survey sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                               /clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
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100.0%; Pred. No. 33;
tive 0; Mismatches 0; Indels
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/clone="CH230-400N17"
/db_xref="taxon:9615"
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Matches 21; Conservative
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RESULT 11
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Pan troglodytes MTNRIA gene, VIRTUAL TRANSCRIPT, partial sequence,
SUGNETIC SULVEY SEQUENCE.
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1 (bases 1 to 669)
Clark, A.G., Glanowski, S., Nielson, R., Thomae, P., Kejariwal, A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X. H., White, T. J., Sninsky, J. J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                       Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
                                                                                 AY405330 869 bp DNA linear GSS 16-DEC.
Homo sapiens MINRLA gene, VIRTUAL TRANSCRIPT, partial sequence.
                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 869)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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100.0%; Pred. No. 34;
ive 0; Mismatches 0; Indels
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Science 302 (5652), 1960-1963 (2003)
14671302
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    .869
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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/locus_tag="HCM2188"
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                                                                                                                                genomic survey sequence.
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AY405331.1 GI:39761305
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Best Local Similarity
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                                                                                                       DEFINITION
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AY405331
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AY405330
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/clone="INAGE:471020"
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/lab_host="Bh108 (T1 phage-resistant)"
/clone="Inha MGC 76"
/clone="Inha MGC 76"
/clone="Inha MGC 76"
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Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGAGACATG-dT(30)BN-3' (where B = A,
C, or G and M = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Cgapbs-romail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
Thissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1548 row: k column: 18
High quality sequence stop: 502.
Location/Qualifiers
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Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria,
1 (bases 1 to 1023)
2 (bases 1 to 869)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 34;
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100.0%; Pred. No. ...
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="MTNR1A"
/locus_tag="HCM2188"
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Best Local Similarity luv...
Local 21; Conservative
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DEFINITION

LOCUS

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 12 CF661120

Dp

Matches

ORIGIN

ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

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/mol type="mrkha"
// Add type="mrkha"
// Add type="mrkha"
// Add type="mrkha"
// Add type="germinal center B cell"
// Iab host="DH10B"
// Add type="germinal center B cell"
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// provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
// Add Add Marti (CBRR). CDNA synthesis was
// Add Add Not I - Oligo (AT) primer
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                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 251)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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271 bp DNA linear GSS 05-OCT-200
IM0325H05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0325H05 R, genomic survey sequence.
AZ491769
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 245.
Location/Qualifiers
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Railly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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    similar to contains Alu repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

    .251
    /organism="Homo sapiens"

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                                            AA250969
AA250969.1 GI:1885930
                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
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                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF661120 aRNA linear EST 07-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Addrews. Cossins
Contact: Addrews. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4510
Fax: +44(0)151-795-4510
Fax: +44(0)151-795-431
Fax: +44(0)151-795-431
Fax: +41(0)151-795-431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Liver"
/dev stage="Adult"
/lab_host="2.coli Electromax DH10B"
/clone lib="Carp liver library 5"
/note="Vector: pTriplEx2; Site_1: Sfil GGCCATTACGGCC; Site_2: Sfil GGCCCTCGGCC; Serially subtracted cDNA challenged animals"
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gracey, A.Y., Fraser, E., Li, W. and Cossins, A.R. Microarray and EST analysis of the carp (Cyprinus carpio) transcriptome during environmental stress Unpublished (2003)
                                                                                                                                                                                                                       ö
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                                                                                                                                  Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 21; DB 14; Length 1103;
                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
CA). Note: this is a NIH_MGC Library."
                                                                                                                         Score 21; DB 12;
Pred. No. 34;
                                                                                         1.8%; Scor.
100.0%; Pred. No. 5...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 21; DB 1
Best Local Similarity 100.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .1103
/organism="Cyprinus carpio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:7962"
/clone="33n22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyprinus carpio (common carp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male & female"
                                                                                                                                                                                                                                                                                                       150 TAATTATTTTTTTT 170
                                                                                                                                                                                                                                                                                                                                                                                    720 raarrarrirrirriri 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 AATGCTCTTGGAATTCCTGCT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AATGCTCTTGGAATTCCTGCT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33n22 5', mRNA sequence.
CF661120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF661120.1 GI:37558249
                                                                                                                                                                                                              21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyprinus carpio
                                                                                                                    Query Match
Best Local Similarity
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source

FEATURES

DEFINITION

RESULT 13 AA250969 LOCUS

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Gaps

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GSS 05-OCT-2000

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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMAP12014|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 279)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tags from cabernet sauvignon berries at various developmental stages developmental stages (nonbulished (2003), Contact: Douglas Cook, PhD CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLJO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Wector: PWD4Zly; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAB70005_IIIaF_B07_Cabernet_Sauvignon_Berry_Post-Veraison - CAB7_Vitis vinifera_CDNA_clone_CAB70005_IIIaF_B07_5', mRNA_sequence.
CB981626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Score 20; DB 28; Length 271;
100.0%; Pred. No. 97;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0325 row: H column: 05
Seg primer: CACACAGGAAACAGCTAATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                   Clāss: plasmid ends
High quality sequence stop: 271.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0325H05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 TTTGATTTCCATTCCTCTGT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 rirgarirccarrccicis 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB981626.1 GI:30304832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                 USA
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                                                                                   84112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
CB981626/c
                                                                                                                                                                                                                                                                                                                                                          Source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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à g JOURNAL

COMMENT

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/done lib="Caberner Sauvignon Berry Post-Veraison - CAB7"
/done lib="Caberner Sauvignon Berry Post-Veraison - CAB7"
/note="Corgan: Berry; Vector: pDNR; Site 1: Sfil; Site 2:
Sfil; CAB7 is a cDNA library of Caberner Sauvignon Clone 8
berries. Samples were collected post-veraison from
field-grown vines during stage III of berry growth at 89
days after full bloom. Berries soluble solid concentration
ranged between 18-19 brix. Sampled vines were located at
the University of California, Davis, Experimental
Vineyard. cDNss were made by oligo-dr priming and directi
onally cloned. 5'and 3' adaptors were used in cloning as
follows: S'-ARGCGGGCGGARGAGTGGCCATTACGGCGGG-3' and
5'-ATTTACAGGCCGGCAATGAT(3H) NO.3'. Library was
constructed using the Clontech Creator SWART kit and
size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 14; Length 279; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Post-Veraison, 18-19 brix"
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                            /organism="Vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Email: drcook@ucdavis.edu
Seg primer: ACGGTACCGGAATATGCC.
                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:29760"
/clone="CAB70005_IIIaF_B07"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
1./*; Journal J. 97;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 1, 2004, 18:37:41
Job time: 3527 secs
                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 TGCCTTCAAAGTGGGTTCCT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 recerreaagregerreer 42
                                                                                                                                                                                                                                           source
                                                                                                                                                                                                     FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 1, 2004, 10:05:02 ; Search time 59 Seconds (without alignments) 1872.476 Million cell updates/sec Run on:

US-10-626-445-8 Title: Perfect score:

2048 1 MSESNSTGILPPAAQVPLAF.......WKILCVTKWPALSQNQSVSS 391 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp201s:*
geneseqp201s:*
geneseqp2003s:*
geneseqp2003bs:* A Geneseq 29Jan04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		þ				
No.	Score	Query Match	Query Match Length DB	DB	ID	Description
٦	2035	99.4	391		AAM50565	Aam50565 Monse his
7	1745	85.2	391		AAM50566	Pat hi
Э	1370.5	66.99	390		AAB02831	
4	1370.5	6.99	390	'n	AAY71297	Human
Ŋ		6.99	390		AAB62445	
9		6.99	390		AAG64477	7 Human
7		6.99	390	4	AAB73622	Human G
80	1370.5	6.99	390		AAM53050	Hilman
o	1370.5	6.99	390	S	ABP98629	Himan hi
10	1370.5	6.99	390	2	ABB78276	Amino
11	1370.5	6.99	390	Ŋ	AAM50564	Human
12	1370.5	6.99	390	Ŋ	AAG66023	Нишап
13	1370.5	6.99	390	Ŋ	AAU74906	Amino
14	1370.5	6.99	390	9	ABG71960	Human
15	1370.5	6.99	390	9	ABU92265	Human
16	1370.5	6.99	390	9	ABP81727	7 Human hi
17	1370.5	6.99	390	9	AAE36417	Human
18	1370.5	6.99	391	S	AAM53052	Human
19	1370.5	6.99	392	Ŋ	AAM53053	Human
20		66.7	390	4	AAM51410	Human
21	1366.5	66.7	390	9	AAE36416	Himan
22	1238	60.4	389	ഹ	AAM50567	Guinea
23	9	58.5	357	9	AAE36415	
24	_	52.5	336	ø	AAE36414	
25	729.5	32.6	415	7	AA029530	Human

Aaw92975 Human mAC Aay06322 Human G p Aag67830 Human mus	Human A huma Human		ADP01687 Human his ADP74567 Kuman his ADP76405 Human mus ADD59931 Human his	Human Human Human	Human Novel Monkey Monkey
AAW92975 AAY06322 AAG67830	AAY92218 AAB30627 ABB79792	ABK4366/ ABP57425 AAO19746 ABD81687	ABG74567 ABG76405 ABP59931	AAO29527 ADD22854 AAY22208	AAB15381 ABG12680 ABR43668 ABP57426
01010	W 4 70 /	.	φφφ	r r 2	m 4 0 0
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35.3		3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	35.3 35.3	35.3 35.1 35.1
722.5	722.5	722.5	722.5	722.5 722.5 722.5	722.5 719.5 718.5 718.5
26 27 28	330 31 31	1 60 60 4 60 44 70	337	39 4 4 1 1	4 4 4 4 4 4 4 4 4 4 4 4 3 3 4 3 4 4 4 4

ALIGNMENTS

WO200192485-A1

06-DEC-2001.

22-FEB-2001; 2001WO-US005914.

31-MAY-2000; 2000US-0208260P.

(ORTH) ORTHO-MCNEIL PHARM INC.

Liu C; Lovenberg T,

WPI; 2002-114339/15. N-PSDB; AAI70981.

encoding it is New mammalian histamine H4 receptor proteins and polynucleotides the proteins, useful in gene therapy for treating diseases where beneficial to elevate mammalian histamine H4 receptor activity.

Claim 13; Fig 5B; 92pp; English.

The present sequence is that of a mouse histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAN10980-83) and polypeptides (see AAN50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the trearment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful

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                                                                                                                                                                                         DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                         for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                                                                                                                                                                                                                                                                                 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLAIS
                                                                                                                                                                                                                                             SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
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                                                                                                                                           1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy.
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0
                                                                                          Length 391;
                                                                                        Score 2035; DB 5; Length 3
Pred. No. 1.9e-202;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PICHREGKAFWKILCVTKQPALSQNQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM50566 standard; protein; 391 AA
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                                                                                            99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat histamine H4 receptor.
                                                                                                        Best Local Similarity 99.7
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lovenberg T, Liu C;
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N-PSDB; AAI70982.
                                                                    Sequence 391 AA;
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The present sequence is that of a rat histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA clubtype, as predicted from a cDNA clone isolated from a spleen cDNA clubtype, as predicted from a cDNA clone isolated from a spleen cDNA clibrary. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAA10980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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beneficial to elevate mammalian histamine H4 receptor activity
                                                                                                                                                                                                                                                                                                                                                                               Length 391;
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                                                                                                                                                                                                                                                                                                                                                                              85.2%; Score 1745; DB 5;
84.9%; Pred. No. 2.6e-172;
ive 17; Mismatches 42;
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                                   Claim 13; Fig 6A; 92pp; English.
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Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                 Sequence 391 AA;
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239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                     MILEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening; transmembrane receptor; signal cascade.
                                                                              179 SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
                                                                                                       PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG
                                                                                                                                                                           RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY
                                                                                                                                                                                                                                Human orphan G protein-coupled receptor hRUP7.
                                                                                                                                                                                                                 PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS 391
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99US-0123946P.
99US-0123949P.
99US-0136436P.
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99US-0136439P.
99US-0135567P.
99US-0137127P.
99US-0141448P.
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990S-0156634P.
990S-0156634P.
990S-0157281P.
990S-0157281P.
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                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000 (first entry)
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N-PSDB; AAD01124.
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28-MAY-1999;
29-JUN-1999;
29-SEP-1999;
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01-OCT-1999;
01-OCT-1999;
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28-MAY-1999;
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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                          The present invention describes transmembrane receptors, preferably human grottein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct adontication of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.9%; Score 1370.5; DB 3; Length 390; 68.1%; Pred. No. 2.1e-133; ive 40; Mismatches 82; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chalmers DT, 12 K, White C;
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                                                                                                   99US-0121852P
99US-0123944P
99US-0123944P
99US-0123948P
99US-0123948P
99US-0123949P
99US-013643P
99US-0136439P
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99US-0137127P
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99US-0151114P
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98US-0109213P.
98US-0110060P.
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                                                                                      99US-0120416P
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267; Conservative
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N-PSDB; AAA46023
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         13-OCT-1999;
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03-SEP-1999;
29-SEP-1999;
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29-SEP-1999;
01-OCT-1999;
01-OCT-1999;
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28-MAY-19
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Best Local S
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The present amino acid sequence is the hRUP7, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned by TF-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. The mendogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and their endogenous ligands, and to screen potential GPCR agonists and their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in the latty and pathological states
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This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-013, encoded by CDNA of NCIMB 41073. The PFI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of FFI-013 are useful in the manufacture of a medicament for treating allergic disorder, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstital and other pulmonary disease, including chronic obstructive pulmonary disease. (COPD), infectious, inflammatory disease, such as inflammatory bowel disease and neoplastic and wyeloproliferative diseases. They are also useful for treating observatives, metabolic, neurological diseases, psychotherapeutics, urogenital disease, reproduction and sexual medicine, psychotherapeutics, urogenital disease, reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, photoageing, skin pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The PFI-013 protein and nucleic acid are useful in the diagnosis and treatment of the above conditions and also for screening drug candidates for the treatment of diseases associated with signal transduction. The antibodies are also useful for enrichment of the account of the contribution and for diseases.
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                                                                                                                                                                                                                                                                                                                           New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
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protein in biological samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.9%; Score 1370.5; DB 4; Length 390; 68.1%; Pred. No. 2.1e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 44; 66pp; English.
                                                                                               29-OCT-1999; 99GB-00025641.
20-APR-2000; 2000GB-00009973.
                                                      24-OCT-2000; 2000EP-00309364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 267; Conservative
                                                                                                                                                                                                                            O'reilly MA;
                                                                                                                                                                                                                                                                   WPI; 2001-309854/33.
N-PSDB; AAF83203.
                                                                                                                                                             (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                   02-MAY-2001
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241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                                                                                                                                                                                       AAB73622 standard; protein; 390
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(SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of the human G protein-coupled receptor protein BG26, which shows significant homology with histamine H3, with activity of binding to histamine and capable of changing intracellular CAMP concentration in response to its stimulus. The protein is applicable as a tool in screening ligands or drug candidates for regulating signal transduction from such protein and treating diseases associated with its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
                                                                                                                                                                                                                Human; G protein-coupled receptor protein BG26; histamine H3; histamine; altering intracellular cAMP concentration; regulating signal transduction.
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                                                                                                                                                                                      Human G protein-coupled receptor protein BG26.
                 359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
361 PLCHRRFOKAFWKILCVTKWPALSQ-NOSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohta M;
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                                                                                                 AAG64477 standard; protein; 390
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                                                                                                                                                          (first entry)
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N-PSDB; AAH47911.
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                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                           25-SEP-2001
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                                                                      RESULT 6
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301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myocardial infarction; stroke; ulcer; migraine; voniting;
psychotic disorder; neurological disorder; anxiety; schizophrenia;
psychotic disorder; neurological disorder; anxiety; schizophrenia;
manic depression; bipolar disorder; depression; delixium; dementia;
severe mental retardation; dyskinesia; Parkinson's disease;
Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
macrophage; eosinophil; neutrophil; function modulation;
autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
drug screening; signal transduction; transgenic animal; drug discovery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel G-protein coupled receptor polypeptide and polymucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.
                                                                                             299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    histamine H3 receptor homologue; infection; viral; bacterial; fungal; protozoan; HTV-1; HTV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoxis;
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                                                                                                                                                    391
                                                                                                                                                                                           359 PLCHKRFOKAFLKIFCIKKOPLPSQHSRSVSS 390
                                                                                                                                                  PLCHRRFOKAFWKILCVTKWPALSQ-NOSVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human G protein-coupled receptor AXOR35.
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contrary to nave. innections; pain; causeis; benny protection; diabetes; obesity; anorexia; bullaid; osteoporosis; asthma; allergies; crimary retention, acute heart failure; hypotension; hypertension; and innertion; stroke; ulcers; mycaralne; vonditing; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental certardarion, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins and antibodies may be useful as vaccines, and AXOR35 proteins and continuation of the string asthma, and inhibiting or promoting the particularly useful for treating asthma, and inhibiting or promoting the particularly useful for treating asthma, and inhibiting or promoting the cuseful for diagnosing or determining susceptibility of an individual to a sthmatic lung. AXOR35 proteins, uncleotides are also useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or via the detection of abnormal levels of protein or wis considered as also useful for inducing an immunological response in a mammal against the above diseases, and for antibodies are useful for trading conditions are also useful as diagnostic reagents, in chromosome localisation and tissue expression studies, and for producing transgenic animals useful in drug corresponding conditions associated with the expression of the AXOR35 protein. The present corresponding corresponding conditions associated with the expression of the AXOR35 protein. The present or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; \$

Sequence 390 AA;

2 360 120 120 240 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALROREYAELLRG 300 SASTEVPASFHSERQRRKSSLMFSSRTKONSNTIASKWGSFSQSDSVALHQREHVELLRA 298 9 9 MILEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN SFLEFVIPVILVAYFNMMIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 1 MSESNSIGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS 1 MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRIERPKSVWYSIAFWLQWFNSFVNPFLY 3; Gaps DB 4; Length 390; Indels Query Match 66.9%; Score 1370.5; DB 4; Best Local Similarity 68.1%; Pred. No. 2.1e-133; Matches 267; Conservative 40; Mismatches 82; 359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390 PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS 391 61 121 181 179 241 301 361 61 121 qq g 원 à d ò 셤 Š 셤 g à ઠે ò

Human G protein-coupled receptor nGPCR-2067. AAM53050 standard; protein; 390 (first entry) 26-MAR-2002 AAM53050 RESULT 8 AAM53050

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Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor; signal transduction; mental disorder; central nervous system disease;

metabolic disease; infection, HIV-1; HIV-2; pain, neurological disorder; psychotic disorder; Huntington's disease; schizophrenia; migraine; depression; anxiety; bipolar disorder; dementia; Alzheimer's disease; Parkinson's disease; proliferative disorder; cancer; psoriasis; benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia; thyroid disorder, cardiovascular disease, hypotension; bybsily; anote thyroid disorder; cardiovascular disease, hypotension; hypertension; thyroid disorder; cardiovascular disease, hypotension; hypertension; inflammatory conditions; autoimmune disorder; rheumatoid arthritis; hormonal disorder; renal failure; anti-HTV; analgesic; cytostatic; antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant; antiatherosclerotic; neuroleptic; antimigraine; antiatherosclerotic; neuroleptic; antimigraine; anticonvulsant; antinflammatory; antirheumatic; antiathritic; Transmembrane_domain_5 /label= Transmembrane domain 6 /label= Transmembrane_domain_1 /label= Transmembrane_domain_2 Transmembrane_domain_3 Transmembrane domain 4 /label= Transmembrane_domain_7 antipsoriatic; gene therapy; receptor. Location/Qualifiers 194 /label= Tr-305 .360 .146 .110 /label= /label= WO200185793-A2. Homo sapiens Domain Domain Domain Domain Domain Domain Domain Κeγ

15-NOV-2001

08-MAY-2001; 2001WO-US014750.

08-MAY-2000; 2000US-0203108P

(PHAA) PHARMACIA & UPJOHN CO

Wood LS;

Vogeli G,

Sejlitz T,

Lind P,

2002-062240/08

N-PSDB; ABA02496.

encodes the novel G polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encoprotein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).

Claim 31; Page 63; 100pp; English.

This sequence represents a novel human G protein-coupled receptor (GPCR) C designated nGPCR-2067. Like all GPCRS, nGPCR-2067 has 7 putative cransmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-2067, to antibodies specific for nGPCR-2067, to drug screening methods c that use nGPCR-2067 and to modulators of nGPCR-2067 activity. nGPCR-2067 invention also discloses the use of nGPCR-2067 activity. nGPCR-2067 and species homologues and may also be used in genetic mapping. The cinvention also discloses the use of nGPCR-2067 nucleic acids in screening c invention also discloses the use of nGPCR-2067 nucleic acids in screening c invention as of species of mappers of these disorders. nGPCR-2067 nucleic acids in screening c acids may additionally be used to generate transgenic acids in cluding c acids may and may provide an insight into treating a variety of human disorders, and may also be used in the design of antisense c molecules for suppressing expression of nGPCR-2067, notelled in conditions, particularly mental disorders, central nervous system conditions, particularly mental disorders, central nervous system

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nervous system, neurological and psychotic disorders such as Huntington's disease, schizophrenia, migraine, depression, anxiety, bipolar disorder, dementia, Alzheimer's disease, and Parkinson's disease, proliferative disorders such as cancers, benign prostatic hypertrophy and psoriasis; metabolic disorders such as diabetes, dyslipidaemia, obesity, and annoexais, thyroid disorders; cardiovascular diseases such as hypotension, hypertension, thrombosis, myocardial infarction, cardiomyopathies, and atherosclerosis, inflammatory conditions; autoimmune disorders (e.g., rheumatoid arthritis); hormonal disorders; and renal failure
                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                               SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; histamine receptor; chromosome 18; anti-inflammatory; anti-allergic; dermatological; cerebroprotective; stroke; anti-mataine; cardiant; atti-rheumatic; anti-arthritic; antipsoriatic; anti-arthritic; antipsoriatic; neuroprotective; inflammation; asthma; allergy; atopic dermatitis; myocardial infarction; migraine; chronic obstructive pulmonary disease; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 SASTEVPASFHSERORRKSSLMFSSRTXMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
 infections, particularly HIV-1 or HIV-2 infections; pain; central
                                                                                                                                                                                                                                                                                                    1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                                                                                         61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                66.9%; Score 1370.5; DB 5; Length 390; 68.1%; Pred. No. 2.1e-133; ive 40; Mismatches 82; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human histamine receptor SP9144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP98629 standard; protein; 390
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                                                                                                                                                                                                                                                Best Local Similarity 68.18
Matches 267; Conservative
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                                                                                                                                                                                                Sequence 390 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                    Query Match
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DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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                                                                                                                                                                                                                                                            This sequence represents the amino acid sequence of a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromatography, in immunoassay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYLLAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SASTEVPASFHSERQRRKSSLMFSSRTKANSNTIASKAGSFSQSDSVALHQREHVELLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYRAQHIGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY
                                                                                                                                                                               for preparing antibodies, e.g. for treating-histamine related
                                                        SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                        Umland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 390;
                                                                                                                                                          New nucleic acid encoding antigenic part of human histamine
                                                      Morse KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.9%; Score 1370.5; DB 5 Best Local Similarity 68.1%; Pred. No. 2.1e-133; Matches 267; Conservative 40; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of human histamine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                    Monsma FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 27-30; 19pp; English.
                                                    Laz TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; protein; 390
                                                  Hedrick JA,
              (SCHE ) SCHERING CORP
                                                                                                      WPI; 2002-442063/47
                                                                                                                         N-PSDB; ABZ80663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 390 AA;
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                                              Behan JX,
                                                                                                                                                                                              disorders.
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178 240

241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAEILLRG 300

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The present sequence represents a histamine receptor. The polypeptide is useful as an antipoen to elicit the production of antibodies. It is useful as an antipoen to elicit the production of antibodies. The histamine receptor polypeptide and polymuclectide are useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD), rheumation arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP), calcium, inositol phosphate and mitogen activated protein (MAP) kinaes), tanges in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+mobilization, mitogenic effects, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel mammalian histamine receptor polypeptide useful for identifying agonist or antagonist for treating diseases such as inflammation, asthma, stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
         Human; histamine receptor; receptor; inflammation; asthma; allergy; atopic dermatitis; stroke; myocardial infection; migraine; chronic obstructive pulmonary disease; COPD; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease; psoriasis; inflammatory bowel disease; psoriasis; intracellular second messenger pathway; cellular growth rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Umland SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Morse KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.9%; Score 1370.5; DB 5; 68.1%; Pred. No. 2.1e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monsma FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 16-17; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laz TM,
                                                                                                                                                                                                                                          19-MAR-2001; 2001US-00812216.
                                                                                                                                                                                                                                                                          99US-00414010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sehan JX, Hedrick JA,
                                                                                                                                                                                                                                                                                                           BEHAN J X.
HEDRICK J A.
LAZ T M.
MONSMA F J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-673827/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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UMLAND S P.
                                                                                                    hormone secretion.
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                                                                                                                                                                       JS2002098539-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  WANG S.
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                            07-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                           (MONS/)
(MORS/)
(UMLA/)
(WANG/)
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(LAZT/)
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5 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240 9 9 DELVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT Gaps ٠. س Length 390; 82; Indels 19 61 121

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The present sequence is that of a human histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA clone interact.

Ilbrary. The invention provides mammalian human, mouse, rat and guinea polypeptides (see AAMSOS64-67). The mucleic acids have been expressed in peramacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 ceceptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing treating or preventing atchma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASRWGSFSQSDSVALHQREHVELLRA 298
                                                                                RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Histamine H4 receptor; human; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy.
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                                                                                                                                               361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS
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                                                                                                                                                                                                                                                       AAM50564 standard; protein; 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2000; 2000US-0208260P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2001; 2001WO-US005914.
                                                                                                                                                                                                                                                                                                                                                               Human histamine H4 receptor
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Best Local Similarity 68.13
Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                               181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
                                                                                                                                                                                          241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                           61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIVLISYDRYLSVSNAV 120
                                                                                                                                                                                                        239 SASTEVPASFHSERQRRKSSLMFSSRTKWNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive; antiasthmatic; antiallergic; neuroprotective; antidiabetic; human; cerebroprotective; cAMP modulator; gene therapy.
                                             DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV
             301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY
                                                                                                                                                                                                                                                              299 RRLAKSLAILLGUFAVCWAPYSLFTIVLSFYSSATGPKSVWYRLAFWLQWFNSFVNDLLY
MSESNSTG1LPPAAQVPLAFIMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                           179 SFLEFVIPVILVAYFNMNIYWSLMKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
                                                                                                                                                                                                                                                                                                       PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                                                                                                                                                                                                                                         PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            AAG66023 standard; protein; 390 AA
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2000US-0227567P.
2000US-0247855P.
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23-AUG-2000;
13-NOV-2000;
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The invention provides an isolated histamine receptor, H4, which binds ligands comprising imidazole attached to amine by an alkyl chain. The H4 receptor can be expressed by standard recombinant methodology. Cells expressing H4 receptor protein at a detectable level can suppress cyclic expressing H4 receptor protein at a detectable level can suppress cyclic adenosine monophosphate (cAMP) formation when contacted with the H4 receptor and antibodies are used for identifying treeptor amodulators. Modulation of histamine H4 receptors is useful to treating transplanted organ rejection, asthma, allergies and cutoimmune pathologies such as multiple sclerosis, type I diabetes, the unmatoid arthritis, cognitive and memory defects. The h4 receptor protein and nucleic acids are useful targets to identify drugs that are protein and nucleic acids are useful targets to identify drugs that are cfetetive in treating disorders associated with histamine-regulated processes. Identification and isolation of H4 receptor provides for development of screening of molecules that interact with H4 receptors. CC development of screening of molecules that interact with H4 receptors. CC development of screening of molecules that interact with H4 receptors. CC development of screening of molecules that interact with H4 receptors. CC development a disorder associated with the function of H4 in peripheral blood received with receptor proviews. The present sequence represents the human histamine H4
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                                                                                             histamine receptor, termed H4 useful for detecting H4 (ant)agonists treating transplanted organ rejection, asthma, allergy, multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.9%; Score 1370.5; DB 5 68.1%; Pred. No. 2.1e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Mismatches
  Pausch MH;
                                                                                                                                       sclerosis and rheumatoid arthritis.
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                                                                                                                                                                           Claim 5; Fig 1; 66pp; English
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Blatcher M,
                                     2002-049442/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor protein
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Jones PG,
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The present invention relates to a new G-protein coupled receptor (GPCR) colypeptide comprising greater than 70% amino acid sequence identity to polypeptide comprising greater than 70% amino acid sequence of human GPCRs TGR21, TGR219.1, TGR130.1, TGR130.2, human TGR213 or TGR22, 80% amino acid sequence identity to mouse TGR18 or 50% amino acid sequence identity to human novel edg receptor protein, as cefined in the specification. The GPCR covalently linked to a solid phase is useful for identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases curinary abnormalities, renal tubule defects, hypertension and curinary abnormalities, renal tubule defects, hypertension and complicated disorders and others. Modulation of the polypeptide of infiltrations, lesions, functional disorders and jaundice and spleencassociated disorders and others. Modulation of the polypeptide of disorders in the present amino acid sequence represents the human GPCR Credits protein coupled receptors of the invention. This sequence is one of seven novel G protein coupled receptors of the invention (AAU74904-AAU74911)
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Amino acid sequence of human G-protein coupled receptor TGR62 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease,
                                                                                           signal transduction modulator; cerebral cavernous malformation; hyperlipidemia, obesity; dyslexia, cardiac myxoma, renal failure, nephritis; hypertension; liver disease; cirrhosis; blood disorder; spleen-associated disorder; immune disorder.
                                                                   G-protein coupled; receptor; GPCR; TGR62; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 390;
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; Pred. No. 2.1e-133;
40; Mismatches 82;
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68.1%;
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267, Conservative
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                                                                                                                                                                                                                                                                            Homo sapiens
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Matches
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Human, receptor; G-protein coupled receptor; AXOR35; lymphocyte; macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastric ulcer; inflammatory bowel disease; crohn's disease; irritable bowel syndrome; vomiting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; renal ischaemia; arteriosclerosis; atherosclerosis; psychosis; neurological disorder; migraine; anorexia; anxiety; schizophrenia; dyskinsor's disease; concer; obesity; stroke; septic shock; and a cancer; cancer; obesity; stroke; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.
                                                                                                                                                          358
179 SFLEFVIPVILVAYFNANIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
                                                  PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                                                                                        RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide, AXOR35, (and its homologues and variants) and its encoding polynucleotide (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or
                                                                        239 SASTEVPASFHSERQRRKSSLMFSSRTKWNSNTIASKMGSFSQSDSVALHQREHVELLRA
                                                                                                                                            The invention relates to an isolated G-protein coupled receptor
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                                                                                                                                                                                              361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                 graft versus host disease; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-protein coupled receptor AXOR35.
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1, Zhu Y;
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                                                                                                                                                                                                                                                                                                                        ABG71960 standard; protein; 390
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20-OCT-2000; 2000US-00693761.
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D, Morrow DM,
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Michalovich
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181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240

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Tymphocytes, macrophages, eosinophils or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist to entagonist identified is useful for treating a disease such as about or inhibiting or promoting the function of lymphocytes. The asthmat, or for inhibiting or promoting the function of lymphocytes. Cathmat, or for inhibiting or promoting the function of lymphocytes.

Cathmatic lung. AXOR35 or polymucleotide is useful in diagnostic assays, or identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such as gastric ulacy, inflammatory bowel diseases (such as remains), unclogical diseases (such as urinary retention), allergy, autoimmune disorders (such as rheumatoid arthritis, cardiovascular diseases (such as urinary retention), hypotension, pulmonary disorders (such as chronic obstructive pulmonary carteriosclerosis, atherosclerosis, gusch as renal ischaemia), arteriosclerosis, anorexia, anxiety, schizophrenial, dyskinesias (such as marcatismors) and seases (such as renal ischaemia), and seases (such as marcatismors) and seases (such as renal ischaemia), earteriosclerosis, anorexia, anxiety, stroke, septic shock, graft warmary and osteoporosis. The present sequence represents
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antagonists of AXOR35 and inhibiting or promoting the function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.9%; Score 1370.5; DB 6; Length 390; 68.1%; Pred. No. 2.1e-133; ive 40; Mismatches 82; Indels 3;
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Best Local Similarity 68.1%
Matches 267; Conservative
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for

Novel endogenous, orphan, human G protein-coupled receptors useful identification of modulators of the receptor and as research tools understanding the role of the receptor in human body.

Claim 26; Page 23; 54pp; English

Lin I;

Liaw CW,

Dang HT,

WPI; 2003-428952/40.

N-PSDB; ACA93262.

990S-0123946P. 990S-0123949P. 990S-0136436P. 990S-0136437P.

28-MAY-1999; 28-MAY-1999;

12-MAR-1999 12-MAR-1999

99US-0121852P

36-JUN-2001; 2001US-00875076

US2003017528-A1

23-JAN-2003

99US-0136567P. 99US-0137127P. 99US-0137131P.

28-MAY-1999; 28-MAY-1999; 28-MAY-1999; 28-MAY-1999; 29-JUN-1999;

99US-0141448P. 99US-0156333P. 99US-0156555P. 99US-0156634P.

99US-00417044

29-SEP-1999; 29-SEP-1999; 12-OCT-1999;

28-SEP-1999

CHEN R. DANG H T. LIAW C W.

(DANG/)

CHEN/)

(FINI/) Chen R,

```
The invention relates to a human G protein-coupled receptor (GPCR)

appearing as ABU92259-ABU92277 (encoded by CDNAs ACA93256-ACA93274) named

hARE-3. hARE-4. hARE-5. hRUP3. hRUP5, hRUP7, hRUP7, hGPCR27, hARE-1. hARE-

-2, hPPR1, hG2A, hCHN4, hCHN4, hCHN6, hCHN9, hCHN10 and hRUF4.

Also included are a plasmid comprising a vector and one of the CDNAs above and a host call comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, gonists or partial agonists. In vitro and in vivo systems incorporating care as understanding the role of constitutive activation as it applies to as understanding the signalling cascade. The CDNAs are useful for making a complex of constitutive activation as it applies to understanding the signalling cascade. The CDNAs are useful for making a probe for doc-blot analysis against tissue mRNA and/or RT-PCR identification of the expression of the invention it issue samples. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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haRE-5; hRUP3; hRUP5; hRUP7; hGPCRZ7; haRE-1; haRE-2; hPPR1; hG2A;
hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUF4; signalling cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G protein-coupled receptor hRUP7.
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120 120 9 9 1 MSESNSTGILPPAAQVPLAFIMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS 61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 61 DFFVGVISIPLYIPHTLEEMDFGKEICVFWLTTDYLLCTASVXNIVLISYDRYLSVSNAV 121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 3; Gaps 66.9%; Score 1370.5; DB 6; Length 390; 68.1%; Pred. No. 2.1e-133; .ive 40; Mismatches 82; Indels 3; ద à

Homo sapiens

16-JUL-2003 ABU92265;

RESULT 15 ABU92265

Search completed: October 1, 2004, 10:11:32 Job time: 64 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October

1, 2004, 10:10:33 ; Search time 18 Seconds
(without alignments)
1121.431 Million cell updates/sec

US-10-626-445-8

Title: Perfect score: Sequence:

1 MSBSNSTGILPPAAQVPLAF.......WKILCVTKWPALSQNQSVSS 391

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 segs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq Maximum DB seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Issued Patents AA:*

(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2. Appli	2	Sequence 2. Appli	Sequence 30. Appl				N	10	2	2	Segmence 2. Appli		25		Sequence 10. Appl	Semience 20. Appl	Sequence 20, Appl	
US-08-334-698-2	US-08-228-932-2	US-08-468-939-2	US-08-722-001-30	US-08-406-855A-2	US-08-722-190-2	US-08-244-354-2	US-09-206-899-2	US-09-444-783-2	US-09-688-415-2	US-09-444-783-2	PCT-US95-04203-2	US-09-688-415-9	US-08-722-001-25	US-09-032-742-5	US-09-688-415-10	US-08-406-855A-20	US-09-206-899-20	
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388.5	388.5	388.5	388.5	388.5	388.5	388.5	388.5	388.5	388.5	388.5	388.5	387.5	386.5	385.5	385.5	385	385	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

```
APPLICANT: Behan, Jiang Xu
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Haz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Mnland, Shelby P.
APPLICANT: Wind, Shelby P.
TILLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION UNDHER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
Sequence 2, Application US/09414010
Patent No. 6204017
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-414-010-2
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 390
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3; Gaps ; Score 1370.5; DB 3; Length 390; ; Pred. No. 7.2e-106; 40; Mismatches 82; Indels 3; 82; Indels Query Match
Best Local Similarity 68.1%;
Matches 267; Conservative 46

61 DFFVGVISIPLYIPHILFEWDFGKEICVFWLATDYLLCTASVYNIVLISYDRYLSVSNAV 120 120 121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240 241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300 09 09 1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS 61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWL/TDYLLCTASVYNIVLISYDRYQSVSNAV ò Db ò qq à g ò Db ò

RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFUNPFLY 360

301

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239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASRWGSFSQSDSVALHQREHVELLRA 298

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NUMBER OF SEQUENCES:
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US-09-165-543-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
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    299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
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APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.9%; Score 1370.5; DB 4; Lengua
68.1%; Pred. No. 7.2e-106;
Mismatches 82; Indels
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                                                   359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                  PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                        APPLICANT: Laz, Thomas M.
APPLICANT: Monsma, Krederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Undland, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
TITLE PEFERRNCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR PILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08985090
Patent No. 5885893
                                                                                                                                    Sequence 2, Application US/09812216
Patent No. 6613533
                                                                                                                                                                                APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                    GENERAL INFORMATION:
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214 VTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPBAQPSPPPPGCWGCWGKGHGBAMPLH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AGPSTISSSASGHLHRAGVACRISNPGLKESAASRHSESPRRKSSILV 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVWPFLYPLCHRRFQKAFWKI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 GLCWARYTLLMIRAACHGHCVP-DYWYETSFWLLMANSAVNPVLYPLCHHSFRRAFTKL 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 722.5; DB 2;
; Pred. No. 4e-52;
51; Mismatches 116;
                                                                                                                                                                                                                                                                      & COCKFIELD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.3%;
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                      445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 38.8%
Matches 165; Conservative
               E: LAHIVE & CO
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-985-090-2
CORRESPONDENCE ADDRESS:
                                                            Massachusetts
: USA
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCPOK 431
                                              CITY: Boston STATE: Massac
                                                                                                                                                                                                                            FILING DATE:
                                                                                           02109
                ADDRESSEE:
STREET: 28
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                                                                              COUNTRY:
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ORGANISM: Artificial Sequence
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                                        427 LCPOK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 LCVTK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCPQK 431
                                                                                                                                                 RESULT 5
US-09-167-354-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-642-855-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------WSLWKRRALSRCPSH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 RYGVGEAAVGAEAGEATLGGGGGG----GSVASPTSSSG----SSSRGTERPR----- 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AGFSTISSSASGHLHRAGVACRISNPGLKESAASRHSESPRRKSSILV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 SLRTHMNSSITAFKVGSFWRSESAALRQR------EYAELLRGRKLARSLAILLSAF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSLAVIVSIF 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||||| | |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 LAFLMSSFAFAIMVGNAVVILAFVVDRNIRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
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Sequence 2, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD, LLP
STREET: 22 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 445 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 ALCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPFLYPLCHRRFOKAFWKI 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 ------AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILV 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 LLVWVLAFILYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                        TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3 TITLE OF INVENTION: SUBTYPE FILE REFERENCE: JWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.3%; Score 722.5; DB 3; Length 445; Best Local Similarity 38.8%; Pred. No. 4e-52; Matches 165; Conservative 51; Mismatches 116; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-167-354-7
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
Sequence 7, Application US/09167354A
Patent No. 6136559
GEMERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Parlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
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Patent No. 6413743
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Exlander, Mark
APPLICANT: Pyati, Jayashree
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216
SEQ ID NO 7
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JAPLICANT: LOVENDECT, Timothy

APPLICANT: Briander, Mark

APPLICANT: Briander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne

TITLE OF INVENTION: SUBTYPE

TITLE OF INVENTION: SUBTYPE

TITLE OF INVENTION: NUMBER: US/09/642,514

CURRENT APPLICATION NUMBER: US 09/167,354

PRIOR FILING DATE: 2000-08-21

PRIOR FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0
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      APPLICAMT: HUVAT, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
TITLE OF INVENTION: SUBTYPE
                                                                                                                                                                                                                                                                                                                                 93;
                                                                                                                                                                                                                                                                                               35.3%; Score 722.5; DB 4; Length 445; 38.8%; Pred. No. 4e-52; tive 51; Mismatches 116; Indels 93
                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
                                                   FILE REFERENCE: JWW
CURRENY PAPPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEY: 2.0
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Patent No. 6437100
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                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                Similarity
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Best Local Simi
Matches 165;
                                                                                                                                                                                     LENGTH: 445
TYPE: PRT
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214 VTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPPGCWGCWGKGHGEAMPLH 273
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                                                                                                                                                                                      93; Gaps
                                                                                                                                            445;
                                                              ; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE US-09-642-514-7
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Receptors and Uses Therefor
                                                                                                                                            Length
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                       Query Match 35.3%; Score 722.5; DB 4; Best Local Similarity 38.8%; Pred. No. 4e-52; Matches 165; Conservative 51; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 VAYFNVQIY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-165-543-5
Sequence 5, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl an TITLE OF INVENTION: Muscarinic Recipies OF SEQUENCES: 39
CORRESPED: LAHIVE & COCKFIELD, I.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PAROR APPLICATION DATA:
APPLICATION NUMBER: 09/0-
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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144 LVWVLAFLIYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFESV 200
                                                                                                                                                               193 AYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHS 252
                                                                                      138 AVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYLLTITMLLEFLLPVISY 192
                                                                                                                                                                                                      -----RLDGAREAAGPEPPEAQPSPP 239
                                                                                                                                                                                                                                      253 ESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELL-RGRKLARSLAILL 311
                                                                                                                                                                                                                                                                 ----GCW------GCWQKGHGEAMPLHRKVAKSLAVIV 270
                                                                                                                                                                                                                                                                                                              312 SAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRREQKAF 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08985090
Patent No. 5885893
BENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/985,090
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.4%; Score 582.5; DB 2; Best Local Similarity 37.7%; Pred. No. 1.3e-40; Matches 137; Conservative 45; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD, STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMES: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                  201 TFFNLSIYLNIQRRTRL-
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COUNTRY: USA
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                             240 PPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ESAASRHSESPRRKSSILVSLRTHM 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 NSSITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 XPSASSASLEKRMKMVSQSITQR--FRLSRDKKVAKSLAIIVSIFGLCWAPYTLLMIIRA 382
                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                          63; Gaps
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                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.2%; Pred. No. 1.3e-51;
Matches 165; Conservative 54; Mismatches 128; Indels 63
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38.3%; Pred. No. 7.1e-44;
tive 44; Mismatches 110; Indels
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TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
FILE REFERENCE: GP-70681
CURRENT APPLICATION NUMBER: US/09/524,162
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASISEQ for Windows Version 3.0
NAME: Elizabeth A. Hanley
REGISTATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)22-7400
TELEFRAM: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Patent No. 6355452
GENERAL INFORMATION:
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                                                                                                                                                LENGTH: 445 amino acids
TYPE: amino acid
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Best Local Similarity 38.3
Matches 141, Conservative
                                                                                                                                                                                                MOLECULE TYPE: protein
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US-09-524-162-2
                                                                                                                                                                                            linear
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LENGTH: 351
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257 RKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAFAI 316
                                                                                                                                                                                                                                                                                   317 CWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILC 376
                                                                                                                                                                                                                                                                                                                                                     287 CWAPYTLIMIRAACHGRCIB-DYWYETSFWLLWANSAVNPULYPLCHYSFRRAFTKLLC 345
                                                                                                                                                                                                                61 AQQGDTRRAVRKMALVWVLAFLLYGPAIL---SWBYLSGGSSIPBGHCYAEFFYNWYFLI 117
                                                                                                                                            118 SASTLEFFTPPLSVTFFNLSIYLNIQRRTRLRLDGGREAGPEPPDAQPSPPAPPSCWG 177
                                                                                                                                                                                            ----ESAASRHSESPR 256
                                                    124 AQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYILT 178
                                                                                                                          --SRCPSHAGFSTIS 222
Sequence 13, Application US/08118270

Sequence 13, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                223 SSASGH----LHRAGVACRTSNPGLK------
                                                                                                                             179 ITMLLEFLLPVISVAYFNVOIYWSLWKRRAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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202-737-3528
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 348 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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TELEFAX: 2
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US-08-118-270-13
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                                                                                                                                                                                                                                                                                                                                   AQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILT 178
                                                     -----ESAASRHSESPR 256
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Sequence 32, Application US/09165543

Patent No. 6093545

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.4%; Score 582.5; DB 3; Length 37.7%; Pred. No. 1.3e-40; tive 45; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/165,543 FILING DATE: CLASSIFICATION:
                                                                                                                                                                            223 SSASGH----LHRAGVACRTSNPGLK----
                                                                                                          179 ITMLLEFLLPVISVAYFNVQIYWSLWKRRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPRAX: (617)742-4214
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APPLICATION NUMBER: 09/042,780
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Best Local Similarity
Matches 137; Conserv
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STATE: Massacl
COUNTRY: USA
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US-09-165-543-32
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REGISTRATION NUMBER: 34,033
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ATTORNEY/AGENT INFORMATION:
                                                           Query Match
Best Local Similarity 27.9%
Matches 109; Conservative
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INFORMATION FOR SEQ ID NO:
           // MOLECULE TYPE: peptide
PCT-US93-08528-13
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MEDIUM TYPE: Floppy
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D.C.
USA
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STATE: D
COUNTRY:
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                                                                                                                                          76 VLF--NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GI 129
                                                                                                                                                                | :| | :| | :| | :| | 122 MIGIA-----WLISFILWAPAILC---WQYLVGKRIVPIDECQIQFLSEPTITFGTAIAA 173
                                                                                                                                                                                                              130 MKIVAQMVAVWILAFLVNGPMILASDSW-----KNSTNTKDCEPGFVTEWXILTITMLLE 184
                                                                                                                                                                                                                                                                                          -- RALSRCPSHAGFSTTSSSASGHLH 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAGVACRISNPGLKESAASRHSESPRRKSSILVSLRIHMNSSITAFKVGSFWRSESAALR 290
                                                                                                              61
                                                                                          16 VPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPH
                                                                                                                                                                                                                                                                                                                  174 FYIPVSIMRILYCRIYRETEKRTKDLADLQGSDSVYKAEKRKPAHRA------LF
                                          86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
CORRESPONDENCES: 348
CORRESPONDENCE ADDRESS:
     Length 348;
Query Match
20.8%; Score 427; DB 1; Length 34
Best Local Similarity 27.9%; Pred. No. 9.1e-28;
Matches 109; Conservative 76; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEB: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                  351 FNSFVNPFLYPLCHRRFQKAFWKILCVTKW 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      185 FLLPVISVAYFNVQIYWSLWKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MOT
TELECOMMUNICATION
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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COUNTRY: USA
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76 VLF--NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GI 129
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                                                                                                                                                                                                                                                                                                                                        130 MKIVAQMVAVWILAFLVNGPMILASDSW----KNSTNTKDCEPGFVTEWYILTITMLLE 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 OREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRIERPKSVWYSIAFWLQW 350
                                                                                                                                                                           61
                                                                                                           16 VPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPH
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                               96;
     Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 FYIPVSIMRILYCRİYRETEKRTKDLADLOGSDSVYKAEKRKPAHRA--
20.8%; Score 427; DB 5; Length 34: 27.9%; Pred. No. 9.18-28; rive 76; Mismatches 119; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING ADPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 INSTVNPICYALCNRTFRKTFIMLLC--RW 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 RSCLRCPRPIKGLNPNPS--HOMIKRKRMS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 FNSFVNPFLYPLCHRRFQKAFWKILCVTKW 380
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLPVISVAYFNVQIYWSLWKR----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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202-737-3528

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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 KESAASRHSESPRRKSSILVSIRTHMNSSITAFKVGSFWRSESAALRQREYAELLRGRKL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARSLAILLSAFAICWAPYCLFTIVLSTYPRIERPKSVWYSIAFWLQWFNSFVNPFLYPLC 363
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                                                                                                                                                                                                                                                                                                                                           133 VAOMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYILTITMLLEFLL 187
                                                                                                                                                                                                                                                                                                                                                                                                                       -----LQASGTEAETENFVHPTGS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GIMKI 132
                                                                                                                                                                                                                                    18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL 77
                                                                                                                                                                                                                                                               3 IAFLIGILALWITIGNILVIVSFKWNKQLKTVNNYFLLSLACADLIIGVISMNLFITYII 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPPORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                   64;
                                                                                                                                                          Length 355;
                                                                                                                                                        20.8%; Score 427; DB 1; Length 35:
29.6%; Pred. No. 9.3e-28;
tive 75; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PR PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
ADDRESSEE: A19 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRSCSSYELQQQKR----FALKT--RSQITKRKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : :|| :: | | | 175 PVTIMRI----LYWRIYKETE-KRTKELAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 11, Application PC/TUS9308528 ; GENERAL INFORMATION:
                        LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                Query Match
Best Local Similarity 29.6'
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRRFQKAFWKIL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SE | SE | SE | SE | NKTFRTTFKTLL 324
        SEQUENCE CHARACTERISTICS
                                                                                  TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-118-270-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US93-08528-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 FN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GIMKI 132
                                                                                                                                                                                                                                                                                                                                                                                                                   133 VAQMVAVWILLAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYILTITMLLEFLL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 KESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRGRKL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 ARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPFLYPLC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LVKEKKA 253
                                                                                                                                                                                                                                                                                                                             3 IAFLIGILALVITIGNILVIVSFKVNKQLKTVNNYFLLSLACADLIIGVISNNLFTTYII 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN----PGL
                                                                                                                                                                                                                                                                                                  18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                             Length 355
                                                                                                                                                                                                             Query Match 20.8%; Score 427; DB 5; Length 35 Best Local Similarity 29.6%; Pred. No. 9.3e-28; Matches 110; Conservative 75; Mismatches 123; Indels
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                    11
                                                              LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                          PCT-US93-08528-11
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October 1, 2004, 10:11:54; Search time 134 Seconds (without alignments) 938.981 Million cell updates/sec
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1 MSESNSTGILPPAAQVPLAF......WKILCVTKWPALSQNQSVSS 391
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12 (cgn2_6/ptodata/2/pubpaa/DCT_NEW_PUB.pep:*

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14 (cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

15 (cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

16 (cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

17 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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19 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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15 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

16 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

17 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

19 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11 (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

12 (cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

13 (cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

14 (cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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16 (cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1351062 seqs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Sequence 2, Appli	• •	Somioned a, Appli	v -	Sequence 14, Appl	Sequence 14, Appl	Sequence Z, Appli	sednence 629, App	Sequence 14, Appl	Sequence 2, Appli	Sequence 14. Aprol	Seminary 14 April	rdde 'Fr annahaa	Sequence 2, Appli	seduence 14, Appl	Segment C annumble
SUMMARIES	ID	US-09-910-411:2	US-09-852-165-2	US-09-891-138A-6	US-10-349-253A-2	IIS-09-875-076-14	US-09-876-252-14	IIS-10-052-103-2	TR-10-225-503	110-10-223-36/A-623	110 10 214 200 0	US-10-354-769-2	US-10-393-807-14	US-10-417-820A-14	US-10-696-673-2	115-10-723-955-14	110 100 100 111 111 111 111 111 111 111	DS-TD-/3/-PTS-5
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	j Query Match Length DB	390	390	390	390	390	390	390	390	0 0	0 0	000	390	390	390	390	0	000
%	Query Match	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6 99	0.00	,	00	6.99	66.99	66.9	0 99	
	Score	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370 5	100	10.00	1370.5	1370.5	1370.5	1370 5	1
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Segmence 14. April	Semilar CC apriors		Segmence 2, Appli	Semience 2, Appli	Semica 2, Appli	Seguence 2, Appli	Sequence 349, App	Sections 1, Appli	Seguence /, Appil	Sequence 20, Appl				Seductice 5, Appl.1		Sequence 5, Appli	Sequence 3. Appli	Seguence 1 Appli	Semience 3 April	Seminance 32 April	Semience 32, Appt	Semience 32, Appl		Segmence 32, Appl	Sednemee 188, App	Sequence 10, Appl	Sequence 22, Appl	Sequence 82, Appl	Sequence 6, Appli	Sequence 93, Appl	Secretary A society
5 US-10-782-596-14	US-10-290-078-27	US-09-350-206-2	US-09-349-755-2	US-09-166-334-2	4 US-10-282-958-2		US-10-453-106-1				US-09-350-206-5			110 - 00 - 011 - 1				US-09-891-053-1		US-09-350-206-32	US-09-349-755-32	US-09-166-334-32	US-10-282-958-32				US-10-029-009-	US-09-782-980-82	US-09-884-430-6		
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39	39	44	44	445	44	44	445	44	45	44	44	44	44	445	,	44	445	413	441	362	362	362	362	460	478		490	460	460	460	460
6.99	66.7	35.3	35.3	35,3	35.3	35.3	35.3	35.3	35.3	35.1	35.0	35.0	35.0	L L		0.00	35.0	34.6	28.9	28.4	28.4	28.4	28.4	20.2	200		7.07	20.0	20.0	20.0	20.0
1370.5	1366.5	722.5	722.5	722.5	722.5	722.5	722.5	722.5	722.5	718.5	716.5	716.5	716.5	716.5	776 5	110.0	716.5	709.5	591	582.5	582.5	582.5	582.5	413	413	1 .	417	410	410	410	410
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30		7 6	32	33	34	35	36	37	38	39	40		- c	7 4 7	4.3	4	4.

ALIGNMENTS

US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; Patent No. US20020137054A1
; Patent No. US20020137054A1
; Patent No. US20020137054A1
; APPLICANT: Bitzgerald, Laura
APPLICANT: Li, Xiatorg
; APPLICANT: Li, Xiatorg
; APPLICANT: Li, Xiatorg
; APPLICANT: Li, Xiatorg
; APPLICANT: Li, Xiatorg
; APPLICANT: Li, Xiatorg
; APPLICANT: Li, Xiatorg
; APPLICANT: Di, Xiatorg
; APPLICANT: MUMBER: 09/09/910,411
; FILE REFERENCE: 2001-07-20
; FILE REFERENCE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR PILING DATE: 1999-11-02
; PRIOR PLILING DATE: 1999-11-02
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 2
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NOS: 2
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NOS: 2
; SOFTWARE: SASTSEQ for Windows Version 4.0
; SEQ ID NOS: 2
; SOFTWARE: SASTSEQ for Windows Version 4.0
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; SEQ ID NOS: 2
; SORTWARE: SASTSEQ for Windows Version 4.0
; SEQ ID NOS: 2
; SORTWARE: SASTSEQ for Windows Version 4.0
; SEQ ID NOS: 3; CONSERVATIVE 40; Mismatches 82; Indels 3; Gaps
; Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps
; Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps
; Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps
; Matches 100 1 MSESNSTGILPPAAQVPLAFFMSINAFMSNYFFINIAIS 60
; SEQ ID NOS: 2
; MATCHES SEVENTILIAPSTAFFMSINAFMSNYFFINIAIS 60
; SEQUENCE IN MATCHES SEVENTILIAPSTAFFMSINAFMSNYFFINIAIS 60

61 DFLVGLISIPLYIPHVLENWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYOSVSNAV 120

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301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: human TGR62 G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82; Indels
                                                                                                                                                                                                          APPLICANT: Zhao, Jiagang
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030083245A1e1 Receptors
FILE REFERENCE: 018/781-006410US
CURRENT APPLICATION NUMBER: US/09/891,138A
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.9%; Score 1370.5; DB 10;
68.1%; Pred. No. 3.2e-119;
tive 40; Mismatches 82; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                     359 PLCHKRPQKAFLKIFCIKKQPLPSQHSKSVSS 390
           361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10349253A publication No. US20040043393A1 GENERAL INFORMATION:
APPLICANT: AADart, Kelly APPLICANT: Bergsma, Derk APPLICANT: Fitzgerald, Laura
                                                                                                                                   ; sequence 6, Application US/09891138A; Publication No. US20030083245A1; GENERAL INFORMATION: APPLICANT: Lin, Daniel Chi-Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.1%
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-10-349-253A-2
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US-09-891-138A-6
                                                                                                       RESULT 3
US-09-891-138A-6
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                                                          181 MILEFILIPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
                                                                                                                               SYRAQHIGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSINTKDCEPGFVTEWYILII 180
DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
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APPLICANT: Lind, Peter
APPLICANT: Sejlitz, Torsten
APPLICANT: Sejlitz, Torsten
APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20030032784Alel G Protein-Coupled Receptors
FILE REFERENCE: 00231regUS
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: USSN 60/203,108
PRIOR APPLICATION NUMBER: USSN 60/203,108
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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68.1%; Pred. No. 3.2e-119;
ive 40; Mismatches 82; Indels
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Publication No. US20030032784A1
GENERAL INFORMATION:
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Matches 267; Conservative
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ORGANISM: Homo sapiens
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Fublication No. US20030017528A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENGES
CURRENT FILING DATE: 2001-06-06
FRIOR APPLICATION NUMBER: US/09/875,076
PRIOR APPLICATION NUMBER: 09/417,044
                                                     APPLICANT: MALLELY, DAIGHT
APPLICANT: MOTOW, Dwight
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C2
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/10/349,253A
PRIOR FILING DATE: 2001-07-20
PRIOR PAPLICATION NUMBER: 09/693,761
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR PRING APPLICATION NUMBER: 09/491,898
PRIOR FILING DATE: 1000-02-03
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PRIOR APPLICATION NUMBER: 09/491,898
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PRIOR APPLICATION NUMBER: 09/491,898
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Michalovich, David
Graybill, Todd
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Best Local Similarity
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TYPE: PRT
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61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: 1999-05-28

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PRIOR PELING DATE: 1999-02-29

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PRIOR PELING DATE: 1999-02-29

PRIOR PELING DATE: 1999-00-17

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PRIOR PELING DATE: 1999-10-01

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PRIOR PILING DATE: 1999-10-01
      R FILING DATE: 1999-02-16
R APPLICATION NUMBER: 60/121,851
R FILING DATE: 1999-02-26
R APPLICATION NUMBER: 60/123,946
R FILING DATE: 1999-03-12
R APPLICATION NUMBER: 60/123,949
R FILING DATE: 1999-03-12
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R APPLICATION NUMBER: 60/137,127

R FILING DATE: 1999-05-28

R APPLICATION NUMBER: 60/137,131

R FILING DATE: 1999-05-28

R APPLICATION NUMBER: 60/131,448
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/136,437
FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/136,439
FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/136,567
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Matches 267; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 14
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ORGANISM: Homo sapiens
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241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALROREYAELLRG 300
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; Boulication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INFENTION: HISTAMINE RECEPTOR ANTAGONISTS
FILE REFERENCE: PC10863A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR PILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.9%; Score 1370.5; 68.1%; Pred. No. 3.2e
                 PRIOR APPLICATION NUMBER: 60/157,280
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-00-19
PRIOR FILING DATE: 1999-00-19
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PRIOR FILING DATE: 1999-00-19
PRIOR FILING DATE: 1999-00-19
PRIOR FILING DATE: 1999-00-19
APPLICATION NUMBER: 60/156,653
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Best Local Similarity 68.1%
Matches 267; Conservative
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CRGANISM: Homo sapiens
US-10-052-193-2
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, ORGANISM: Homo sapiens
US-09-876-252-14
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LENGTH: 390
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241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALROREYAELLRG 300
              RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lia, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Lian, Landon G Protein Coupled Receptors CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 1999-10-12
PRIOR PILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR PILING DATE: 1999-02-16
PRIOR PILING DATE: 1999-02-16
PRIOR PELING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR PILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR PILING DATE: 1999-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1370.5; DB 14; Lengt; Pred. No. 3.2e-119; 40; Mismatches 82; Indels
                                                                                                                                                                                                                                                   PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/10272983; Publication No. US20030148450A1; GENERAL INFORMATION:
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Matches 267; Conservative
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Sublication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
TITLE OF INVENTION: ANTICENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
CURRENT FILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE PATENTIAN VERSION 3.1
                                                                                                                                                    DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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        DB 13; Length 390;
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                                              Indels
66.9%; Score 1370.5; DB 13
68.1%; Pred. No. 3.2e-119;
ive 40; Mismatches 82;
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                                        Conservative
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; ORGANISM: Homo
US-10-225-567A-629
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                                      267;
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  Query Match
Best Local 9
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APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INTENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOSO
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR PILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,46
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR PILING DATE: 1999-05-28
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68.1%; Pred. No. 3.2e-119;
tive 40; Mismatches 82;
                359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                                                                                                   Sequence 14, Application US/10393807; Publication No. US20030175891A1; GENERAL INFORMATION:
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Best Local Similarity 68.11
Matches 267; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                        APPLICANT: Chen, Ruoping
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ORGANISM: Homo sapiens
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68.1%; Pred. No. 3.2e-119;
.ive 40; Mismatches 82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10354769

Publication No. US20030149242A1

GENERAL INRORMATION:

APPLICANT: Pfizer Inc.

APPLICANT: O'Reilly, Mark A.

APPLICANT: O'Reilly, Mark A.

APPLICANT: Peter, Beate

TITLE OF INVENTION: NOVEL POLYPEPTIDE

FILE REFERENCE: PC10373B

CURRENT APPLICATION NUMBER: US/10/354,769

CURRENT APPLICATION NUMBER: US 09/698,801

PRIOR PILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-06-14

PRIOR PILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1909-10-29

PRIOR FILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-14

PRIOR PILING DATE: 1000-06-16

SOFTWARE: PATENTION NUMBER: GB 0009973.9

SOFTWARE: PATENTING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 2
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267; Conservative
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US-10-354-769-2
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Matches 26
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APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Lind, Peter
APPLICANT: Lind, Peter
APPLICANT: Sejlitz, Torsen
APPLICANT: Sejlitz, Torsen
APPLICANT: Wodeli, Gabriel
APPLICANT: Wodeli, Gabriel
APPLICANT: Wodeli, Gabriel
APPLICANT: Wodeli, Gabriel
APPLICANT: Wodeli, Linda &
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: PHRNODS-10/10/00231REGUS.1 DV1
CURRENT PILING DATE: 2003-10-26
PRIOR APPLICATION NUMBER: US 60/203,108
PRIOR FILING DATE: 2001-05-08
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 390
                   239 SASTEVPASFHSERQRRKSSLMFSSRTKONNSNTIASKONGSFSQSDSVALHQREHVELLRA 298
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                                                                                                                                DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV
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Publication No. US20040105846A1
GENERAL INFORMATION:
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Matches 267; Conservative
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US-10-696-673-2
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US-10-723-955-14
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOWITEZ, KEVIN
APPLICANT: CALIMERS, Derek T.
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: 7.0528.CON
CURRENT PELLING DATE: 3003-04-16
PRIOR PELICATION NUMBER: 09/416,760
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR PELING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-03-12
PRIOR PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR PRIOR APPLICATION NUMBER: 60/123,948
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                                                                                                             359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                            361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                                                             Sequence 14, Application US/10417820A
Publication No. US20030229216A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Lowitz, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: LOWICE, NEVIL F.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
TITLE OF INVENTION: Receptors
FILE REPERENCE: 7.10529.COM
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT APPLICATION NUMBER: 10/417,820
PRIOR APPLICATION NUMBER: 09/116,760
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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PRIOR PELICATION NUMBER: 60/123,948
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                                                                                                                                                Lehman-Bruinsma, Karin
Lowitz, Kevin P.
Dang, Huong T.
Chen, Ruoping
Gore, Martin
Application US/10723955
to. US20040110238A1
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                                                             APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
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Best Local Similarity 68.1'
Matches 267; Conservative
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US-10-723-955-14
      Sequence 14, Applica
Publication No. US20
GENERAL INFORMATION:
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179 SFLEFVIPVILVAYFNRNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
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                                                                                                                                                                                        Sequence 2, Application US/10737619
; Publication No. US20040138234A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; CURRENT APPLICATION NUMBER: US/10/737,619
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2010-10-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2:
; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
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                                                  361 PLCHRRFOKAFWKILCVTKWPALSQ-NOSVSS
                                                                           359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS
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Best Local Similarity 68.1%
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-737-619-2
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1, 2004, 10:07:13 ; Search time 18 Seconds (without alignments) 2089.494 Million cell updates/sec October Run on:

1 MSESNSTGILPPAAQVPLAF......WKILCVTKWPALSQNQSVSS US-10-626-445-8 2048 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	histamine 44 vector	τ			muscarinic acetyle			magarinic acetylo							muscarinic acerylc		carinic a	D3 dopamine recept	alpha-la-adrenergi	d3 dopamine recept	alpha-1-adrenergic	alaba-17-damand	: E	₹:	Take 15 - 4cre		g i		hypothetical prote
SUMMARIES	ID	JC7566	A24325	809508	JT0531	S01114	A29514	151837	S47572	A29476	S10128	B29514	A55019	A31897	110530	571323	A35546	0.0000	THOAA	750100	340491	A41632	I39369	172495	156507	A45121	A38731	٠ ۸	S10126	T18863
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de	Query Match	6.99	20.2			20.0	20.0	20.0			19.7		19.6	6	6	19.2	6	6	. 6	6		19.0	6	8	8	80	ø		18.6	ω.
	Score	0	413	4.	0	410.5	410	41	409.5	403	402.5	402	401	400	б	392.5	392	06	90	89	68	388.5	88	86	85	84	82	382	380.5	80
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ALIGNMENTS

RESULT 1

JC7566 histamine H4 receptor, HH4R - human Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cidate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 Cidate: 30-Jun-2001 #sequence_revision 30-Jun-2001 Cidate: 30-Jun-2001 Rinamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K. Rinakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K. Rinakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K. Rinakamura, T.; Itadani, H.; Hidaka, M.; Ohta, M.; Tanaka, K. Rinakamura, T.; Itadani, H.; Hidaka, M.; Soforman, Soforman, T.; Hidaka, M.; Millani, M.; M.; Millani, M.;	A; Accession: JG7566 A; Molecule type: mRNA A; Residues: 1-390 <nak> A; Residues: 1-390 <nak> C; Coment: This receptor; belonging to the biogenic amine receptors of G protein-coupled C; Gene: hh4r</nak></nak>
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C;Keywords: G protein-coupled receptor; transmembrane protein

Gaps 3; Ouery Match

66.9%; Score 1370.5; DB 2; Length 390;
Best Local Similarity 68.1%; Pred. No. 4.3e-110;
Matches 267; Conservative 40; Mismatches 82; Indels 3;

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DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120 9 09 1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 61 Ωp ò g

120 180 178 121 SYRAQHIGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT à g

181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240 ò q

241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300

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239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASRWGSFSQSDSVALHQREHVELLRA 298 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSLAFWLQWFNSFVNPFLY 360 301 a à q

PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391 361 359 ò g

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JT0531
muscarinic acetylcholine receptor M5 - ra
C;Species: Rattus norvegicus (Norway rat)
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RESULT 2
A24325
muscarinic acetylcholine receptor - pig
c; Species: Sus scrofa domestica (domestic pig)
C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 05-Nov-1999
C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 05-Nov-1999
C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 05-Nov-1999
C; Accession: A24325
R; Kubo, T: Pukuda, K: Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; Hag
Nature 323, 411-416, 1986
A; Attle: Cloning, Sequencing and expression of complementary DNA encoding the muscarinic
A; Meference number: A24325
A; MID: 87014801; PMID: 3762692
A; Accession: A24325
A; Molecule type: mRNA
A; Residues: 1-460 «KUB»
A; Residues: 1-460 «KUB»
A; Residues: 1-460 «KUB»
A; Residues: 1-460 «KUB»
A; Cross-references: GB: XO4413; NID: G1863; PIDN: CAA28003.1; PID: G1866
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
C; Keywords: G protein-coupled receptor; glycoprotein; reansmembrane #status predicted «TM3»
F; 100-121/Domain: transmembrane #status predicted «TM4»
F; 1810-120/Domain: transmembrane #status predicted «TM5»
F; 1867-387/Domain: transmembrane #status predicted «TM5»
F; 1870-180/Domain: transmembrane #status predicted «TM5»
F; 1870-200/Domain: transmembrane #status predicted «TM5»
F; 1870-200/Domain: transmembrane #status predicted «TM5»
F; 1870-200/Domain: transmembrane #status predicted «TM5»
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 21-Jul-2000
C;Date: 31-Dec-1990 #sequence xevision 31-Dec-1990 #text_change 21-Jul-2000
C;Accession: S09508; S06327; S04326
R;Chapman, C.G.; Browne, M.J.
Nhucleic Acids Res. 18, 2191, 1990
A;Atitle: Isolation of the human m1 (Hm1) muscarinic acetylcholine receptor gene B,Reference number: S09508; MUID:90245684; PMID:2336407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YILTITMLLEFILEVISVAYFNVQIYWSLWKR-----RAL----SRCPSHAGFSTTSSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 RSQPGAEGSPETPPĠRCCR----C'RAPRLLQAYSWKBEREEEDBGSMESLTSSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ROREYAEL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 SEVVIKMPMYDPEAQAPAKQPPRSSPNTVKRPTRKGRERAGKGOKPRGKEQLAKRKTFSL 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLVGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SNPGLKESAASRHSESPRRK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.2%; Score 413; DB 2; Length 460; 27.5%; Pred. No. 9.7e-28; rive 83; Mismatches 154; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 FLYPLCHRRFOKAFWKILCVTKW 380
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Best Local S
Matches 122
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A;MOJecule type: DNA
A;Residues: 1-460 <ALLI>
A;Residues: 1-460 <ALLI>
A;Residues: 1-460 <ALLI>
A;Cross-references: GB:Y00508; GB:M35128; NID:g297405; PIDN:CAA68560.1; PID:g297406
B;Across-references: GB:Y00508; GB:M35128; NID:g297405; PIDN:CAA68560.1; PID:g297406
B;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J
EMBO J. 6, 3923-3929, 1987
B;Peralta, E.; Salasse, Selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection of the selection
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                                                                 A, Residues: 1, 1460 CCHA.
A, Residues: 1, 1460 CCHA.
A, Cross-references: EMBL:X52068; NID:g34450; PIDN:CAA36291.1; PID:g34451
A, Cross-references: EMBL:X52068; NID:g34450; PIDN:CAA36291.1; PID:g34451
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
R, Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.
Nucleic Acids Res. 15, 10604, 1997
A, Title: Sequence of the gene encoding the human MI muscarinic acetylcholine receptor.
A, Reference number: S06327; MUID:88096607; PMID:3697105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 RŚQPGAEGSPETPPGRCCR---CĊRAPRLLQAYSWKEEEEEDEĠSMEŚLTŚSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FLUGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SNPGLKESAASRHSESPRRK 258
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A;Cross-references: EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PID:g32318
C;Superfamily: vertebrate rhodopsin
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F;142-168/Domain: transmembrane #status predicted <TM4>
F;142-168/Domain: transmembrane #status predicted <TM5-
F;367-387/Domain: transmembrane #status predicted <TM5-
F;367-387/Domain: transmembrane #status predicted <TM6-
F;402-420/Domain: transmembrane #status predicted <TM7>
F;2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted
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nucleic acid sequence not shown; translation not shown
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20.2%; Score 413; DB 2; L
Best Local Similarity 27.4%; Pred. No. 9.7e-28;
Matches 122; Conservative 84; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Keywords: G protein-coupled receptor; glycoprotein; F.25-50/Domain: transmembrane #status predicted <TMl>F:62-93/Domain: transmembrane #status predicted <TMl>
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INPMCYALCNKAFRDTF-RLLLLCRW 437
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A. Status: preliminary
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C. Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotr
C. Superfamily: vertebrate inhodopsin
C. Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F. 29-52/Domain: transmembrane #status predicted <TM1>
F. 104-125/Domain: transmembrane #status predicted <TM3>
F. 1104-125/Domain: transmembrane #status predicted <TM3>
F. 146-168/Domain: transmembrane #status predicted <TM4>
F. 147-345/Domain: transmembrane #status predicted <TM4>
F. 148-496/Domain: transmembrane #status predicted <TM6>
F. 478-496/Domain: transmembrane #status predicted <TM7>
F. 712/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                             Neuron 1, 403-410, 1968

Affille: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor A; Reference number: UT0530; MUID:90166521; PMID:3272174

A; Accession: UT0531
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A, Molecule type: DNA
A, Molecule type: DNA
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-531 «LIA»
A, Cross-references: GB: M22925; NID: g205311; PIDN: AAA41572.1; PID: g205312; GB: J04706
A, Note: the nucleotide sequence for residues 101-120 and the translation 121-140 are not A, Note: the authors translated the codon CAG for residue 19 as Glu, AAC for residue 65 a B, Kiwttenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C. A, Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues involved the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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A; Residues: 1-531 < BON>
A; Residues: 1-531 < BON>
G. F.: Themmen, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, M.; Birnbaumer, L.
G. Biol. Chem. 264, 7328-7337, 1989
A; Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor.
A; Reference number: A33354; MUID:89214170; PMID:2540186
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C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 21-Jan-2000 C;Accession: JT0531; A33354; C37121 R;Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
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20.0%; Score 410.5; DB 2;
Best Local Similarity 24.6%; Pred. No. 1.9e-27;
Matches 122; Conservative 92; Mismatches 140;
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Musicarinic acetylcholine receptor M2, glandular - pig
NyAlternate names: muscarinic acetylcholine receptor III
C;Becies: Sus scrofa domestica (domestic pig)
C;Becies: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Feb-2000
C;Accession: S0114
FBS Lett. 235, 257-261, 1988
A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis A;Accession: S01114
A;Molecule type: DNA
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862
C;Superfamily: vertebrate rhodopsin
C;Sepwords: G protein-coupled receptor; glycoprotein; neurotransmitter zeceptor; transmembrane #status predicted <TM1>
F;68-91/Domain: transmembrane #status predicted <TM2>
F;143-164/Domain: transmembrane #status predicted <TM3>
F;185-207/Domain: transmembrane #status predicted <TM3>
F;185-207/Domain: transmembrane #status predicted <TM4>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;331-522/Domain: transmembrane #status predicted <TM5>
F;528-546/Domain: transmembrane #status predicted <TM6>
F;528-546/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
442 TLSAILLAFIITWTPYNIMVLV-STFCDKCVPVTLWH-LGYWLCYVNSTINPICYALCNR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REYAELLRGRKLARSLAILLSAFALCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWF 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LRQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 VAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYLLTIMLLEFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LA-----WVISFILWAPALL---FWQYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STTSSSASGHLHRAGVACRTSNPGLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 PVIIMII----LYWRIYKETE-KRIKELAGLQASGTEAAENFVHPTGSSRSCSSYELQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 QSLKRSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.0%; Score 410.5; DB 2; Length 590; 24.8%; Pred. No. 2.1e-27; Live 82; Mismatches 136; Indels 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HSES---
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                                                       366 RFQKAFWKILCVTKW 380
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-590 <AKI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 SAASR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 125;
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Best Local
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Rilai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske, Adv. Exp. Med. Biol. 287, 313-330, 1991
A;Title: The molecular properties of the MI muscarinic receptor and its regulation of cyt A;Reference number: I51837; MUID:92101806; PMID:1759615
A;Accession: I51837
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C,Species: Bos primigenius taurus (cattle)
C,Species: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Feb-2000
C,Accession: S47572
C,Accession: S47572
B,Cohim: Biophys. Acta 1223, 151-154, 1994
A,Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re
A,Teference number: S47572, MUID:94339178; PMID:8061048
A,Accession: S47572
A,Setuus: preliminary
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 FLUGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SNPGLKESAASRHSESPRRK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 RSQPGAEGSPESPPGRCCR---CCRAPRLLQAYSWKEEEEEDEGSMESLTSSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSILVSL------ALRQREY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 SEVVIKMPMVDSEAQAPTKOPPKSSPNTVKRPTKKG---RDRGGKGCKPRGKEQLAKRKT 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                 muscarinic receptor - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: I51837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 NITVLAPGKGPWQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSLACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 YILTITMLLEFLLPVISVAYFNVQIYWSLWKR----RAL----SRCPSHAGFSTISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 NSTGILPPRAQVPLAFL---MSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:S73971; NID:g241253; PIDN:AAB20705.1; PID:g241254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.0%; Score 410; DB 2; Length 46 27.4%; Pred. No. 1.7e-27; Aative 83; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437
413 VNPMCYALCNKAFRDTF-RLLLLCRW 437
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A; Residues: 1-460 <RES>
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                                                   MASSIA accetylcholine receptor M1 - rat
muscarinic acetylcholine receptor M1 - rat
muscarinic acetylcholine receptor M1 - rat
C, Species. Rattue norvegicus (Norway rat)
C, Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C, Accession: A94518; A94293; A37121; A29514
R; Bonner T I 1980 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C, Accession: A94518
A; Rocerece number: A94518
A; Rocerece number: A94518
A; Residues: 11-460 - 280.
A; Residues: 11-460 - 280.
A; Reterner number: A94293; MIJD:87263421; PMID:3037705
A; Picher J Garilla type: mRNA
A; Residues: 12-727333-409
A; Picher J Garilla C, Border
A; Reterner number: A94293
A; Picher J Garilla C, Border
A; Reterner number: A94293
A; Picher J Garilla C, Border
A; Reterner number: A94293
A; Picher J Garilla C, Border
A; Reterner number: A37233-409
A; Reterner number: A37233-409
A; Reterner number: A37233-409
A; Reterner number: A37233-409
A; Reterner number: A37233-409
A; Reterner number: A37231
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A; Reterner number: A3723
A; Reterner number: A3723
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A; Reterner number: A3723
A; Reterne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLVGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYRAQHTGIMKIVAQMVAV-WILAPLVNGPMILASDSWKNSTNTK----DCEPGFVTEW 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YILTITMELEFELPVISVAYFNVQIYWSLWKR-----RAL----SRCPSHAGFSTTSSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SNPGLKESAASRHSESPRRK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 RSQPGAEGSPESPPGRCCR---CCRAPRLLQAYSWKEEEEEDEGSMESLTSSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 SSILVSL-----ALRORES 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 NITVLAPGKGPWQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSLACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.0%; Score 410; DB 2; 27.4%; Pred. No. 1.7e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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84; Mismatches 145;
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Best Local Similarity 24.0%
Matches 121; Conservative
                125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S10128
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                Matches
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C,Superfamily: vertebrate rhodopsin

C,Superfamily: vertebrate rhodopsin

C,Superfamily: vertebrate rhodopsin

C,Superfamily: vertebrate receptor; glycoprotein; neurotransmitter receptor; transme

F;67-90/Domain: transmembrane #status predicted <TM1>

F;104-124/Domain: transmembrane #status predicted <TM2>

F;184-206/Domain: transmembrane #status predicted <TM4>

F;230-251/Domain: transmembrane #status predicted <TM5>

F;492-512/Domain: transmembrane #status predicted <TM6>

F;527-545/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norregicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476; MUID:88077068; PMID:3120722
                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                  245
                                                                                                                                                                                                                              78 FN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GIMKI 132
                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                     191 LA-----WVISFILWAPAİL---FWQYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYM 242
                                                                                                                                                                                                                                                                                                                                                                                              254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 QSMKRSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSFQKSFSKLPIQLESAVDTAKASDVNSSVGKTTATLPLSFKEATLAKRFALKTRSQITK 477
                                                                                                                                                                              18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                    133 VAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG-----FVTEWYILTITMLLEFLL
                                                                                                                                                                                                                                                                                                                                                                       188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STTSSSASGHLHRAGVACRTSNPGLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEEELGSVGLERKPSKLQTQQSMDDG
              A;Cross-references: EMBL:U08286; NID:g520465; PIDN:AAA51866.1; PID:g520466
                                                                                        20.0%; Score 409.5; DB 2; Length 590;
25.0%; Pred. No. 2.6e-27;
.ive 83; Mismatches 134; Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M18088; NID:g202657; PIDN:AAA40659.1; PID:g202658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 403; DB 2; Length 589; Pred. No. 9.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------HSES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 ---PRRKSSILVSLRTH---MNS----SITAFKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 GSFWRS-----ESAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSFVNPFLYPLCHRRFQKAFWKIL 375
                                  C; Superfamily: vertebrate rhodopsin C; Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.7%;
23.8%;
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               246 SAASR----
                                                                                                          Similarity
A;Residues: 1-590 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-589 < BRA>
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Best Local Similarity
                                                                                                     Best Local Sim
Matches 126;
                                                                                         Query Match
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A;Residues: 1-590 cPRs.
A;Cross-references: EMBL:X15266; NID:g32323; PIDN:CAA33337.1; PID:g32324
C;Cuperfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen F;68-95/Domain: transmembrane #status predicted cTM1.
F;105-131/Domain: transmembrane #status predicted cTM2.
F;143-164/Domain: transmembrane #status predicted cTM3.
F;185-207/Domain: transmembrane #status predicted cTM4.
F;231-252/Domain: transmembrane #status predicted cTM6.
F;493-513/Domain: transmembrane #status predicted cTM6.
F;525-546/Domain: transmembrane #status predicted cTM6.
F;525-546/Domain: transmembrane #status predicted cTM7.
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R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expre
                                                                                                                                                      59 ISDFLVGLISIPLYIPHVLFN-WNFGSGLCMFWLITDYLLCTASVYNIVLISYDRYQSVS 117
                                                                                                                                                                                        118 NAVSYRAQHT----GIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG---- 169
                                                                                                                                                                                                                                                                                                         278 NFVHPTGSSRSCSSYELQQQGVKR---SSRRKYGRCHFWFTTKSWKPSAEQMDQDHSSSD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 SWNNNDAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSSILNSTKLPSSDNLQVSNED 394
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                                                                              4 SNSTGILPPAAQ-----VPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLA
                                                                                                                                                                                                                                                                                                                                                                               -FVTEWYILTITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STISSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 LSFKEATLAKRFALKTRSQITKRKRMSLIKEKKAAQTLSAILLAFIITWTPYNIMVLV-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Species: Homo sapiens (man)
Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 LGTVDVERNAHKLQAQKSMGDGDNCQKDFTKLPIQLESAVDTGKTSDTNSSADKTTATLP
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SSILVSLRTHMNSSI----
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  172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TAFKVGSFWRSESAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 TYPRIERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKIL 375
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 GHLHRAGVACRTSNPGLKESAASRHSESPRRK-----
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76 VLE-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GIM 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273
              15;
                                                                                                                                                                                                                                                                                                                             -FVTEWYILTITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STISSSAS 226
                                                                                                                                                                                                                                                                                                                                                           258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IRQREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 NAVSYRAQHT----GIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG---- 169
                                                                                  ISDELVGLISIPLYIPHVLFN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscarinic acetylcholine receptor, M3 isoform - chicken muscarinic acetylcholine receptor, C.Species: Gallus gallus (chicken) C.Species: Gallus gallus (chicken) C.Species: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000 C.SAccession: A.Soller, J.B. R.Gabbut, A.P.: Galper, J.B. J. Biol. Chem. 269, 25823-25829, 1994 A.Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick A.R.Eference number: ASS019; MUID:95014393; PMID:7929287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 VPLAFLMSSFAFRAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPH
                                                                                                                                                                                                                                                                  395 IGTVDVERNAHKLQAQKSMGDGDNCQKDFTKLPIQLESÄVDTGKTSDTNSSADKTTATLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SSILVSLRTHMNSSI-----
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                                                      SNSTGILPPAAQ-----VPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross_references: GB:L10617; NID:g530097; PIDN:AAA65961.1; PID:g530098 C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate receptor C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cch
al Similarity 24.4%; Pred. No. 1.5e-26;
124; Conservative 84; Mismatches 136; Indels 164;
              Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TAFKVGSFWRSESAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKIL
                  84; Mismatches 145;
Pred. No. 1.1e-26,
                                                                                                                                                                                                                                                                                                                                                                                                                           GHLHRAGVACRTSNPGLKESAASRHSESPRRK----
23.8%;
                  125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-639 <GAD>
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A55019
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Best Local S:
Matches 124,
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                         Matches
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SIPECACEST STATUS NOTVEGICIES (NOVANY TAIL)

C;Species Rattus norvegicus (NOVANY TAIL)

C;Date: 30-Jun-1889 #sequence revision 30-Jun-1889 #text_change 18-Feb-2000

C;Accession: B94518; B94293; B37121; B29514

R;Bonner, T. T.

Submitted to Genmank, July 1987

A;Refidence number: A94518

A;Refidence number: A94518

A;Refidence 1-899 460-1891

B;Bonner, T. T.; Buckley, N.J.; Young, A.C.; Brann, M.R.

A;Residence 1-894518

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                                                                                                                                                                                                                                                                                                                                                                                        357 IGSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEEELGMVDLERKADKLQAQKSVDD 416
                                                                                                                                                                                                                                                                                                                                                                                                                                       ---FWRSESAALR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: | : : | : : | GGSFPKSFSKLPIQLESAVDTAKTSDVNSSVGKSTATLPLSFKEATLAKRFALKTRSQIT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QREYABILRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQW 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : :|| : :|| 243 PVTIMTI----LYWRIYKETEKRIKELAGLQASGTEAETENFVHPTGSSRSCSSYELQQQ 298
                                                                                                                                                                                                                                                                                     VAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYLLTITMLLEFLL 187
    LA-----WVISFVLWAPALL---FWQYFVGKRTVPPGECFIQFLSEPTITFGTALAAFYM
                                                                                                                                                                                                                                                           SSSASGHLHRAGVACRTSNPGLKES
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TAFKVGS-
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Score 402; DB 2; Length 589

19.68;

Query Match

186 LLPVJ 289 YLPVJ 244 KESAR 344 QRQST 260	QY 225 ASGHLHRAGVACRTSNPGLKESAASRHSESPRRK 258 Db 243 RSOPGAEGSPESPPGRCCRCCRAPRILQAYSWKEEEEEDEGSMESLITSSEGEEPG 297 QY 259 SSILVSL
OY 279 GSFWRS 289 	Qy 357 PFLYPLCHRRQXAFWXILCUTKW 380 Db 415 PMCYASCNKAFRDHF-RLLLLCRW 437
OY 290ROREYABILRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFW 347 Db 524 OITKREMSLIERKRAAQTLSAILFAFIITWIPYNIMVLV-NIFCDCV-PKTVW-NLGYW 580 QY 348 LQWPNSFVNPFLYPLCHRRWKLI 375	RESULT 14 JT0530 muscarinic acetylcholine receptor M5 - human C;Species: Homo sapiens (man)
NPVCYALCNKMFRNTFKM NPVCYALCNKMFRNTFKM TO THE TECEPTOR M1 - m S (house mouse) equence revision 2.	C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000 C;Accession. JT0530 R;Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J. Neuron 1, 403-410, 1988 A;Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor A;Accession: JT0530; MUID:90166521; PMID:3272174 A;Accession: JT0530 A;Molecule type: DNA
r. B.A.; Subers, E.M.; Naional expression of the m 21; PMID:2848036	terylcholine rece te rhodopsin coupled receptor; murane #status pr murane #status pr
anslated the codon er, N.M.; Habecker 96, 1989	Fil47-1b9/Jomain: transmembrane #status predicted <tw4> Fil92-214/Jomain: transmembrane #status predicted <tw5> Fi444-464/Jomain: transmembrane #status predicted <tw6> Fi479-498/Jomain: transmembrane #status predicted <tw6> Fi8719-498/Jomain: transmembrane #status predicted <tw7> Fi8.13/Binding site: carbohydrate (Asn) (covalent) #status predicted</tw7></tw6></tw6></tw5></tw4>
i erratum, correct translat: ite rhodopsin coupled receptor; glycoprote embrane #status predicted </td <td></td>	
smembran smembran smembran smembran	31 31 76
Query Match 19.5%; Score 400; DB 2; Length 460; Best Local Similarity 27.0%; Pred. No. 1.3e-26; Matches 120; Conservative 86; Mismatches 152; Indels 86; Gaps 19; Qy 5 WSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLAISD 61	Db 91 ILMGRWALGSLACDLWLALLYVASNASVANLLVISFDRYRSITRPLTYRARRTPRRAGIM 150 QY 131 KIVAQWVAVWILAFLVNGPWILASDSWKNSTWIKDCEPGFVTEWYILTITMILBF 185 LS 1
121 SYRACHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEW	263 QRERNQASWRSSRRSTSTTGKPSQATGPSANWAKAEQLTTCSSYPSSEDEDKPATDPVLQ 245 ESAASRHSESPRKSSILVSLRTHMNSSITAFKVGSFWRSESAALR 323 VVXKSGRESPGREFSARFFEFTEVENTMNNSI
187	

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Libral Adrenergic receptor - Japanese medaka
CiSpecies: Oryzias latipes (Japanese medaka)
CiSpecies: Oryzias latipes (Japanese medaka)
CiSpecies: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
CiAccession: S71323
K: Arsia, S: Emori, Y.

Bur. J. Blochem. 235, 501-507, 1996
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of A;Accession: S71323
A;Reference number: S71323
A;Reference solumary
A;Molecule type: DNA
A;Residuas: 1-471 < 4Rs>
A;Residuas: 1-471 < 4Rs>
A;Cross-references: EMBL: D63859
A;Cross-references: EMBL: D63859
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 AGVACRISNPGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 REYAEL----LRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAF 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 AVSYRAQHTGIMKIVAQMVAVWILAFLVN-GPMILASDSWKNSTNTKD--C----EPGFV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | ::| |::| |::||::||:
138 PLRYPAIMTKRRALLAVML-LWULSVIISIGPLF----GWKEPAPEDETVCKITEBPGYA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 TEWYILTITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHR 231
                                        SLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHR 365
                                                                     4 SNSTGILPP----AAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAI 59
383 LVVKADGNQETNNGCHKVKIMPCPFPVAKEPSTKGLNPNPSHQMTKRKRVVLVKERKAAQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 SNCSHVLAPELNIVKAVVLGMVLGIFILFGVIGNILVILSVVCHRHLQTVIYYFIVNLAV 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 WLGYFNSCINPIIYLCSNQEFKKAFQSLLGVHCLRMTFRAHHHHLSVGQS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.2%; Score 392.5; DB 2; Length 477;
Best Local Similarity 28.0%; Pred. No. 5.8e-26;
Matches 115; Conservative 65; Mismatches 145; Indels 85
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                                                                                                                                       366 RFOKAFWKILCVTKW 380
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501 TFRKTF-KMLLLCRW 514
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 1, 2004, 10:05:12 ; Search time 13 Seconds (without alignments) 1566.110 Million cell updates/sec Run on:

US-10-626-445-8 2048 1 MSESNSTGILPPPAAQVPLAF......WKILCVTKWPALSQNQSVSS 391 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description							DARABO EN CONTRACTOR IN CONTRA	
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	E D	-	-	-	٠,	7	П	Н	-
	Match Length DB	390	445	445	1	440	445	460	532
Query	Match	6.99							
	Score	1370.5	722.5	721	71.0	01.0	715.5	418	414.5
Result	. i	Н	7	m	•	rı	v	9	7

		Description	meines omod 8n8460	Omort Cmod	2001	rattile	P58406 mis misculu	E D E E	Tacaca	homo sa	sus 1	Ĺ	3 sus scr	2 ratt	4	caen	N	mus		O9n2a3 dorilla dor		Dan t	ratt	-	_	orycto		-	Q91175 oryzias lat	gallus	יחטטאפט		TOURS.		tau	
		DI	HH4R HUMAN	HH3R HUMAN	HH3R_CAVPO	HH3R_RAT	HH3R MOUSE	ACM1 MACMU	ACM5 MACMU	ACM1 HUMAN	ACM1_PIG	ACM5 RAT		ACM1 RAT	ACM3 BOVIN	ACM3_CAEEL	ACMS_HUMAN	ACM3 MOUSE	ACM3 PONPY	ACM3 GORGO	ACM3 HUMAN	ACM3 PANTR	ACM3_RAT	ACM1_MOUSE	ACM3_CHICK	A1AD_RABIT	OAR CAEEL	A1AD MOUSE	A1AA_ORYLA	ACM4 CHICK	D3DR_CERAE	D3DR_HUMAN	A1AB MESAU	A1AB_RAT	HH1R_BOVIN	
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,	Query	Match	9	2	35.2	D	4	٠.		20.2			20.0		٠								19.6			19.3					19.1			19.0	19.0	
		Score	1370.5	722.5	721	Н	715.5	418	414.5	Н	41	٠	410.5		409.5	40	404.5	404	403.5	402.5	402.5	402.5	402	401		394.5	393		392.5		O١	w	w	389.5	œ	
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **Subchildurak LUCHILUM: Integral memorane protein.

-!- TISSUB SPECIFICITY: Expressed primarily in the bone marrow and eosinophils. Shows preferential distribution in cells of immunological relevance such as T-cells, dendritic cells, immunological relevance such as T-cells, dendritic cells, mast cells, neutrophils. Also expressed in a wide variety of peripheral issues, including the heart, kidney, liver, lung, pancreas, skeletal muscle, prostate, small intestine, spleen, fetal liver and lymph node. Pregulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

-!- INDUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may faceband on the presence of IL-10 or IL-13.

-!- MISCELLANBOUS: Does not bind diphenhydramine, loratadine, ranitidine, cimetidine, clobenpropit, thioperamide butimamide clozapine, immepip and imetit. The order of inhibitory activity was imetit - clobenpropit > burimamide > thioperamide burimamide closapine behaves as a partial agonist, dimeprim behaves as a full agonist. Thioperamide shows inverse agonism (enhances CAMP activity). The order of inhibitory activity while clozapine behaves as a partial agonism (enhances CAMP activity). The order of inhibitory activity while clozapine behaves was Histamine > N-alpha-methylhistamine > R(-)-alpha-methylhistamine > Both N-alpha-methylhistamine > R(-)-alpha-methylhistamine behave as full
                                                                                                                                                                                                                                                                                                                                                    Puhl H.L. III, Ikeda S.R., Aronstam R.S.; puhl H.L. III, Ikeda S.R., Aronstam R.S.; puhl H.L. III, Ikeda S.R., Aronstam R.S.; sequenced of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: The H4 subclass of histamine receptors could mediate the histamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the
                                                                                                                                                                                                                          Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J., Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L., Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S., Bergsma D.J., Pitzgerald L.R.; Heble P., Wilson S., Bergsma D.J., Pitzgerald L.R.; "Cloning, expression, and pharmacological characterization of a novel human histamine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                       Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR00810275; Histamine_H4.
Pfan; PP600001; 7Fm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                absence of agonist).
SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                Mol. Pharmacol. 59:434-441(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF307973; AAG32052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF312230; AAK12081.1;
AF329449; AAK43542.1;
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Genew; HGNC:17383; HRH4.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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EMBL; AF325356;
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Q9YSNI; Q9GZX2; Q9H4K8;
28-FEB-2003 [Rel. 41, Created)
28-FEB-2003 [Rel. 41, Last sequence update)
15-MAR-2004 [Rel. 43, Last annotation update)
Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
                                                                                                                                                                                                                                                                                                                                                  66.9%; Score 1370.5; DB 1; Length 390; 68.1%; Pred. No. 1.2e-85;
                                                                                                                                                                                                                                                                             S-palmitoyl cysteine (Potential).
A -> V (IN REF. 1).
H -> R (IN REF. 1).
O -> R (IN REF. 1).
C986BBAE7FF912C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            82; Indels
         PRINTS; PR01726; HISTAMINEH4R.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS02527; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                              EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYPOLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PO
                                                                                                                                                                        S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                       CYTOPLASMIC (POTENTIAL).
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A MELLIME LALES 1749; PUDDREGALIYBUDE 2, MELLIME LALES 1749; PUDDREGALIYBUDE 2, MELLIME LALES 1749; PUDDREGALIYBUDE 2, Beloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L., Balley J., Barlow K.F., Barces K.N., Beard L.M., Brown A.J., Basiley J., Barlow K.F., Barces K.N., Beard L.M., Brown A.J., Beasley O.P., Burd C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., A. Cobley V.E., Collier R.B., Connor R.E., Corby N.R., Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Garner P., Gardham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Ammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D., A. Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S. A. March V.L., Martin S.L., McConnachie L.J., McConnachie L.J., McConnachie L.J., McConnachie L.J., McLoy K., McLay K., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.B., Sehra H.K., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wallis M., Wallis J.M., Williams S.A., Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Rocker J., Wallingy D.L., Williams L., Williams S.A., Rocker J., Williams L., Williams L., Williams L., Boerk S., Rocker J., Rocker J., Williams L., Williams L., Broker S., Rocker J., Rocker J., Williams L., Williams L., Williams L., Broker S., Rocker J., Williams L., Williams L., Williams L., Broker S., Rocker J., Rocker J., Williams L., Williams L., Williams L., Williams L., Beck S., Rocker J., Rocker J., Williams L., Williams L., Bentley D.R., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Williams L., Bentley D.R., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J., Rocker J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K., "Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21953383; PubMed=11956964; Wiedemann P., Boenisch H., Oetters F., Bruess M.; "Structure of the human histamine H3 receptor gene (HRH3) and identification of naturally occurring variations."; J. Neural Transm. 109:443-453(2002).
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Ullmer C., Zirwes E., Lubbert H.;
"Cloning and functional expression of the human histamine H3S
                                                                                                                                                                                                                                                                                                                                                  Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J., Huvar A., Jackson M.R., Erlander M.G.; "Cloning and functional expression of the human histamine H3
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20568725; PubMed=11118334;
                                                                                                                                                                                                                                                                                                   MEDLINE=99278519; PubMed=10347254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Thalamus;
MEDLINE=21181559; PubMed=11284713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21638749; PubMed=11780052;
                                                                                                                                                                                                          FROM N.A. (ISOFORM 1).
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iochem. J. 355:279-288(2001)
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                                                                                                        NCBI TaxID=9606;
                                                                                                                                                                                                                                                         TISSUE=Thalamus;
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TESULE SPECIFICITY: Expressed predominantly in the CNS, with the greatest expression in the thalamus and caudate nucleus. The various isoforms are mainly coexpressed in brain, but their relative expression level varies in a region-specific manner. Isoforms 3 and 7 are highly expressed in the thalamus, caudate nucleus and cerebellum while isoforms 5 and 6 show a poor expection. Isoforms 5 and 6 show a high expression in the amygdala, substantia nigra, cerebral cortex and hypothalamus. Section 7 is not found in hypothalamus or substantia nigra. Independent of the syndrome is characterized by orthostatic hypothalamus. The found in hypothalamus or substantia nigra. Independent on bladder and bowel incontinence, anhidrosis, iris arrophy, amyotrophy, ataxia, rigidity and tremor. MISCELLANEOUS: Does not bind to cimetidine and tripolidine. Shows modest affinity for thioperamide, imetit, Nalpha-methylhistamine and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to iodoproxyfan while isoforms 1 and 3 bind it with high affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004969; F:histamine receptor activity; TAS.
GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
GO: GO:0007269; P:neurotransmitter secretion; TAS.
  FUNCTION: The H3 subclass of histamine receptors could mediate the
                   histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist). Agonist stimulation of isoform 3 niether modified adenylate cyclase activity nor induced intracellular calcium
                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                Isold=Q9Y5N1-4; Sequence=VSP_001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9Y5N1-6; Sequence=VSP_001883;
                                                                                                                                                                                                                                                                                                                  Name=3; Synonyms=H3S;
IsoId=09Y5N1-3; Sequence=VSP_001885;
                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9Y5N1-5; Sequence=VSP_001882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9Y5N1-7; Sequence=VSP_001884;
                                                                                                                                                                                                                                                                                                 Isold=09Y5N1-2; Sequence=VSP_001886;
                                                                                                                                                                                                                                                         IsoId=Q9Y5N1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF140538; AAD38151.1; -.
EMBL; AB045369; BAB20090.1; -.
EMBL; AB019000; BAB17030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00001, 7tm 1, 1.
PRINTS; PR00237, GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ296652, CAC51025.1;
EMBL, AJ278250, CAC39434.1;
EMBL, AL078633; CAC04014.1;
EMBL, AF363791; AAK50040.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:5184; HRH3.
MIM; 604525; -.
MIM; 146500; -.
                                                                                                                             mobilization.
                                                                                                                                                                                                                                                                                                                                                                                                           Name=5;
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10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                                                                                            78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAVWILAFLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----WSLWKRRALSRCPSH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILV 263
                                                                                                                                                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                  214 VTFFNLSIYLNIQRRTRLBLDGAREAAGPEPPFFAQPSPPPGGGWGCWQKGHGEAMPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 SLRTHMNSSITAFKVGSFWRSESAALRQR-----EYAELLRGRKLARSLAILLSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKI
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                                                                                                                                                                                                                                                                                                                                                                                                       18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 445;
                                                                                                                                                                                                                                                                                                          TId=VSP 001886.
                                                                                                                                                                                                                                                                                                -> KKMKKKTCL (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                   35.3%; Score 722.5; DB 1; Length 38.8%; Pred. No. 6.5e-42; rive 51; Mismatches 116; Indels
 receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                     -> D (IN REF. 1 AND 5).
2ACF7440FBE9586C CRC64;
          Disease mutation.
EXTRACELLULAR (POTENTIAL)
                                                       EXTRACELLULAR (POTENTIAL)
                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                   LLULAR (POTENTIAL)
                                                                                                                CYTOPLASMIC (POTENTIAL).
                                      CYTOPLASMIC (POTENTIAL).
                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                     /FTId=VSP 001884.
Missing (In isoform 3).
/FTId=VSP 001885.
                                                                                                                                                                                                                                         (in isoform 6).
P 001883.
                                                                                                                                                                                                                                                           Missing (in isoform 7). /FIId=VSP_001984.
                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                      (in isoform 5).
                                                                                                                                                                                                                                                                                                                              012235.
                                                                                                                                                                                                               001881
                                                                                                                                                                                                                                                                                                           /FTId=VSP
                                                                    POTENTIAL.
                                                                                                                                                                                                                                 FTIG=VSP
                                                                                                                          POTENTIAL
                                                                                                                                                                                                               FTIG=VSP
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                                                                                                         POTENTIAL
                                                                                                                                    EXTRACE
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                                                                                                                                                                                                                                                                                                                                                 48671 MW;
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Matches 165; Conservative
G-protein coupled receping Alternative splicing; DOMAIN 1 39
TRANSMEM 40 61 70
DOMAIN 61 70
DOMAIN 92 108
TRANSMEM 109 129
DOMAIN 130 126
TRANSMEM 157 177
DOMAIN 178 196
TRANSMEM 178 196
TRANSMEM 178 196
TRANSMEM 178 196
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256
298
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98
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445 AA;
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360
381
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TRANSMEM
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                                                                                                                                                                                                                                 Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Fillot C., Cochois V., Schwartz J.-C., Arrang J.-M.; Morisset S., Fillot C., Cochois V., Schwartz J.-C., Arrang J.-M.; Fillot Schwartz J.-C., Arrang J.-M.; Morisset S., Fillot Schwartz J.-C., Arrang J.-M.; Fillot Schwartz J.-Fillot Schwarz J.-Fillot Schwarz J.-Fillot J. Subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Long; Synonyms=H3L;
Isold=09J315-1; Sequence=Displayed;
Name=Short; Synonyms=H3S;
Isold=09J155-2; Sequence=VSP_001880;
TISSUE SPECIFICITY: Expressed widely and abundantly throughout the brain. Highly expressed in discrete neuronal populations such as pyramidal cells in cerebral cortex or cerebellar Purkinje cells.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF267537; AAF78947.1; -...

R EMBL; AF267538; AAF78950.1; -...

R InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR0003980; H3_receptor.

PR PRINTS; PR00137; GFCRRHODOPSN.

R PRINTS; PR01471; HISTAMINEH3R.

R PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

R PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.

4 G-protein coupled receptor; Transmembrane; Glycoprotein;

Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                        SUBSCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
             09J135; 090I36;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Histamine H3 receptor (HH3R).
                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
445 AA.
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PRT;
                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=20218440; PubMed=10757514;
 STANDARD;
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61
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 HH3R CAVPO
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us-10-626-445-8.rsp

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                                                                                                                                                                                                                                                                                                                                              214
                                                                                                                                                                                                                                       98 TGRWIFGRGLCKLWLVUDYLLCTSSVFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRRM 157
                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                                                                                   215 VTFFNLSİYLNIQRRTRLALDGGAREAGPDPLPEAQSSPPQPPPGCWGCWPKGQGESMPL 274
                                                                                                                                                                                                                                                                                                                                                                                                       272
                                                                                                                                                                                                                                                                                                                                                                                                                           275 HRYGVGEAGPGAEAGEAALGGGSGAAASPISSSGSSSRGTERPR-----SLKRGSKPS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 ITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 ASSASLEKRMKMVSQSITQR---FRLSRDKKVAKSLAIIVSIFGLCWAPYTLLMIIRAACH 385
                                                                                                                                                                        77
                                                                                                                                                                                   137 VAVWILAFLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILTITMLLEFILPVIS
                                                                                                                                                                                                                                                                                                           158 VLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTFFLS
                                                                                                                                                                                                                                                                                                                                                                                               215 HA-GFSTTSSSA-SGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILVSLRTHMNSS
                                                                                                                                                                  18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                                           ----WSLWKRRALSRCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J., Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.; "High constitutive activity of native H3 receptors regulates histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                         (GLCNAC. . .) (POTENTIAL). (in isoform Short).
                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hypothalamus;
MEDLINE=20330707; PubMed=10869375;
Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
"Cloning of rat histamine H3 receptor reveals distinct species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 RIERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILCVTK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 445
                                                                                                                                        54; Mismatches 133; Indels
                                                                    FTId=VSP 001880.
BAE206A3887189A0 CRC64;
          CYTOPLASMIC (POTENTIAL). POLY-ALA.
                                      N-LINKED (GLCNAC. ...
Missing (in isoform
/FTId=VSP 001880.
                                                                                                            35.2%; Score 721; DB 1; 39.8%; Pred. No. 8.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGOYNG; OGOXNG; OGOXNO; OGOXNO; CB-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Histamine H3 receptor (HH3R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pharmacol. Exp. Ther. 293:771-778(2000)
POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                 48734 MW;
                                                                                                                                                                                                                                                                                                                                        192 VAYFNVQIY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmacological profiles.";
                                                                                                                                        162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:860-864(2000),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
4419
445
24
111
305
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                                                                                 445 AA;
                                                                                                         Query Match
Best Local Similarity
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399
420
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276
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TRANSMEM
DOMAIN
                                        CARBOHYD
                                                                                 SEQUENCE
                                                     VARSPLIC
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                         DOMAIN
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                                                                                                                                                              MOI. Pharmacol. 55:1101-1107(1999).

-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=090YN8-4; Sequence=VSP 001888, VSP 001889;
-!-TISSUE SPECIFICITY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform 1 is largely predominant in all tissues.
-!- MISCELLANEOUS: Proxyfan acts as a potent neutral antagonist while thioperamide, ciproxifan and FUB465 act as potent inverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                             TISSUE SPECIFICITY.
MEDLINE=99279519; PubMed=10347254;
MEDLINE=99279519; PubMed=10347254;
Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
Itadani H., Takimura T., Nakamura T., Ohta M.;
"Cloning of a novel G protein-coupled receptor.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00237, G PROTEIN RECEP F1 1, 1.
PROSITE; PS50262, G PROTEIN RECEP F1 2, 1.
G-protein coupled receptor, Transmembrane; Glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                       SÜBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                      Event=Alternative splicing, Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                        Name=2; Synonyms=H3S;
IsoId=Q9QYN8-2; Sequence=VSP_001887;
                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9QYN8-3; Sequence=VSP_001888;
                                                                                                                                                                                                                                                                                                                                        Name=1; Synonyms=H3L;
Isold=Q9QYN8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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EMBL, AB015646; BAA88766.1; --
EMBL, AB015646; BAA88776.1; --
EMBL, AB015646; BAA88776.1; --
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR003980; H3_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY009370; AAK82086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
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1129
1156
1177
1177
1196
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2217
3380
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3396
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYGVG--EAGPGVEAGEAALGGGSGGGAASPTSSSGSSSRGTERPR-----SLKRGS 324
                                                                                                                                                                                                                                                                                                                                                       VAVWILAFLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS 191
                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of mouse histamine H3 receptor.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist) (By similarity).
                                                                                                    VQPHGSLEQCWK -> CVERLGKLEASLLLPLWMFSGRWRR
RKHVCELDVPWMFNQERQNCRGARGWIGRCGLPRPPPSVLQ
LPAEPRQLLLPAPPPGLGRWPCPACPVCTIRIWGWVVMG
                                                                                         WYETSFWLLWANSAVNPVLYPLCHYSFRRAFTKLLCPQKLK
                                                                                                                                                                                                                                                                157 ALVWVLAFLLYGPAIL---ŚWEYLSGGSSIPEGHĊYAEFFYNWYFLITASTLEFFTPFLS
                                                                                                                                                                                                                                                                                                                                                                                                                             270 NSSITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLS
                                                                                                                                                                                                                                                 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                   ---SRCPSHAGFSTTSSSASGH-----LIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coge F., Rique H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.
Galizzi J.-P.;
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                          /FTId=VSP_001887.
Missing (In isoform 3 and isoform 4).
/FTId=VSP_001888.
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                                                                                                                                                                                                                        63;
                       N-LINKED (GLCNAC. . .) (POTENTIAL) Missing (in isoform 2).
                                                                                                                                                                                                DB 1; Length 445;
                                                                                                                                                                                            ; Score 716.5; DB 1; Length
; Pred. No. 1.7e-41;
54; Mismatches 128; Indels
                                                                                                                                                       FTId=VSP 001889.
63DFEFCZ1758FE5B CRC64;
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histamine H3 receptor (HH3R).
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                                                                                                                                             (in isoform 4)
/FTId=VSP_0018
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                                                                                                                                                                       48588 MW;
                                                                                                                                                                                                35.0%;
                                                                                                                                                                                                             165; Conservative
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305
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274
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P58406;
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            DOMAIN
CARBOHYD
VARSPLIC
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                                                                                                                                                                        SEQUENCE
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                                                                   VARSPLIC
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                                                                                                                                                                                                                Local
  DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 ALVWYLAFLLYGPALL--SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                    SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .) (POTENTIAL)
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PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN.
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EXTRACELLULAR (POTENTIAL)
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SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 715.5; DB 1;
; Pred. No. 1.9e-41;
51; Mismatches 132;
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                         MGD; MGI:2139279; Hrh3.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
                                                                                                                                                                                                                                                                   EMBL; AY044153; AAK72406.1; -.
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40.7%;
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3359
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                  SECUENCE FROM N.A.

TISSUE=Lens epithelium;

TISSUE=Lens epithelium;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE, BREAKDOWN OF PHOSPHOLINOSITIDES & MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Pram; PRO0001; Trai; 1.—
PRINTS; PR00237; GPCRRHDODPSN.
PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS0362; G PROTEIN RECEP F1_2; 1.
POSTSYNAPTIC membrane; Ionic channel; Glycoprotein; Transmembrane;
Phosphorylation; Multigene family; G-protein coupled receptor.

EXTRACELLULAR (POTENTIAL).
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                          (Rel. 36, Created)
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    460 AA
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Muscarinic acetylcholine receptor M1
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InterPro; IPR000276; GPCR_Rhodpsn.
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submitted (SEP-1997) to the EMBL/GenBark/DDBJ databases.
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLAASE, BREAKDONN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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15-JUL-1998 (Rel. 36, Last annotation update)
Muscarinic acetylcholine receptor MS.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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Pfam; PF00001; 7tm_1; 1.
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TISSUE=Lens epithelium;
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84;

83; Mismatches 153; Indels

123; Conservative

Matches

Similarity

Homo sapiens (Human)

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15;
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151 IGLA----WIJSFILWAPAILC---WQYLVGKRTVPLDECQIQFLSEPTITFGTAIAAF
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membrane; Ionic channel; Glycoprotein; Transmembrane;
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CYTOPLASMIC (POTENTIAL).
V-TINKED (GLCNAC. . ) (POTENTIAL).
                   Phosphorylation, Multigene family, G-protein coupled receptor. DOMAIN 1 29 EXTRACELLULAR (POTENTIAL)
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PROSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
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01-NOV-1990 (Rel. 16, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
MUSCARINIC acetylcholine receptor M1.
CHRM1.
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24.5%; Pred. No. 4.40
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i-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                    Eukaryota; Metazoa;
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MIM; 118510; -.

R GO; GO:00058BB7; C:integral to plasma membrane; TAS.

GO; GO:0005624; C:membrane fraction; TAS.

R GO; GO:0004981; F:muscarinic acetylcholine receptor activity; TAS.

R GO; GO:0002831; P:acetyl choline receptor signaling, muscarin. .; TAS.

R GO; GO:0002203; P:cell proliferation; TAS.

R GO; GO:0002203; P:muscarinic acetyl choline receptor, phospho. .; TAS.

R GO; GO:0002203; P:phosphatidylinositol-4,5-bisphosphate hydro. .; TAS.

R GO; GO:0002203; P:protein kinase C activation; TAS.

R GO; GO:000584; P:protein kinase C activation; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

R GO; GO:0001165; P:signal transduction; TAS.

R HIME-PRO; IRRO02276; GPCR Rhodpsn.

R HIME-PRO; IRRO0201; TAM 1; 1.
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PROSITE; PS00237, G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
POSTSYNAPLIC membrane; Ionic channel; Glycoprotein; Transmembrane;
Phosphorylation; Multigene family; G-protein coupled receptor.
DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. . .) (PROBABLE)
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; X15263; CAA33334.1; -.
EMBL; Y00508; CAA68560.1; -.
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460 AA;
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                                  187 IITFGTAMAAFYLPVTVMC----TLYWRIYRETENRARELAALQGSETPGKGGGSSSSE 242
                                                                                                                                                                                                                                           225 AS------GHLHRAGVACRT------SNPGLKESAASRHSESPRRK 258
SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
                                                                                                                               -SRCPSHAGFSTTSSS 224
                                                                                                                                                                                                                                                                                                       243 RŚQPGAEGSPETPPGRCCR---CCRAPRLLQAYSWKEEEEEDEGSMESLTSSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                       | :::: | | : ::: | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 |
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                     175 YILTITMLLEFLLPVISVAYFNVQIYWSLWKR-----RAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-747-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; Ttm_1; 1.
PRINTS; PR00337; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 UNPFLYPLCHRRFOKAFWKILCVTKW 380
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

NCBI_TaxID=10116;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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18;
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                                                                                                                                                                                                                                                                                                           Gaps
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.

EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
VLINKED (GLCNAC. .) (PROBABLE)
N-LINKED (GLCNAC. .) (PROBABLE)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                     Length 460;
                                                                                                                                                                                                                                                                                 20.2%; Score **..,
27.5%; Pred. No. 4.9e-21;
**ive 83; Mismatches 154; Indels
                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
                                                                                                                                           6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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                                                                 EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                             CYTOPLASMIC (POTENTIAL).
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                                                      (POTENTIAL)
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Muscarinic acetylcholine receptor M5.
Rattus norvegicus (Rat).

STANDARD;

P08911;

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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
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                                                                                    SEQUENCE FROM N.A.
BODILINE-20166521; PubMed=1272174;
BODINET I., Young A.C., Brann M.R., Buckley N.J.;
"Cloning and expression of the human and rat m5 muscarinic
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Birnbaumer L.;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                         MEDLINE=89214170; PubMed=2540186;
                                                                                                                                                                                  acetylcholine receptor genes.";
Neuron 1:403-410(1988).
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VLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GIM 130
              131 KIVAQMVAVWILAFLVNGPMILASDSW-----KNSTNTKDCEPGFVTEWYILTITMLLEF 185
                                                                 213
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                                                                                                        -----RALSRCP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88296835; PubMed=3402600;
Akiba I., Macda A., Bujo H., Nakai J., Mishina M., Numa S.;
"Primary structure of porcine muscarinic acetylcholine receptor III
and antagonist binding studies.";
FEBS Lett. 235:257-261(1988).
                                                                                                                                                       ----SHAGFSTT--SSSASGHLHRA-------GVACRTSNPGLKESA-----
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 GSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEBELGTVDLERKASKLQAQKSMDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 GSFOKSFSKLPIQLESAVDTAKASDVNSSVGKTTATLPLSFKEATLAKRFALKTRSQITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82; Mismatches 136; Indels 161; Gaps
PROSITE; PROCEST; G_PROTEIN_RECEP_F1 1; 1.

PROSITE; PSO262; G_PROTEIN_RECEP_F1 2; 1.

POSTSYNAPTIC membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.

EXTRACELLURAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.0%; Score 410.5; DB 1; Length 590; 24.8%; Pred. No. 9.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSFWRS------ESAA------
                                                                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                     e (FOIENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9998D2A4802FD32A CRC64;
                                                                                                                                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------HSES-----
                                                                                                                                                                                                                                         5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                           7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                  1 (POTENTIAL).
                                                                                                                                 2 (POTENTIAL)
                                                                                                                                                                      3 (POTENTIAL)
                                                                                                                                                                                                                                                                              6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLC)
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                   O-LINKED
N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536 NSTVNPVCYALCNKTFRTTFKMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PRRKSSILVSLRTHMN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66077 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                   165
185
208
2230
253
493
514
528
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                                                                                                                                                                                   DOMAIN
TRANSMEM
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TRANSMEM
DOMAIN
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CARBOHYD
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CARBOHYD
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                                                                                              FRANSMEM
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BOVIN
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                                                                                                     MOD_RES
MOD_RES
SEQUENCE
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DOMAIN
TRANSMEM
DOMAIN
                                                   CARBOHYD
DISULFID
                                                                                                                                                       Query Match
Best Local
                                     CARBOHYD
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                                                                                       MOD_RES
                                                                             MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE, BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
                                                                                                      Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P02699; IBOJ.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PR00001; 7; ml; 1.

PRINTS; PR00137; GPCRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS00262; GPROTEIN RECEP F1_1; 1.

PROSITE; PS00262; GPROTEIN RECEP F1_2; 1.

PROSITE; PS00262; GPROTEIN GROEP F1_2; 1.

PROSITE; PS00204; GPROTEIN GROEP F1_2; 1.

Phosphorylation; Multigene family; G-protein coupled receptor.

DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92283857; PubMed=1317867; Savarese T.M., Wang C.-D., Fraser C.M.; Site-directed matagenesis of the rat m1 muscarinic acetylcholine receptor. Role of conserved cystelines in receptor function."; J. Biol. Chem. 267:11439-11448(1992).
                                                                                                                                                             SEQUENCE FROM N.A.
MEDILIBE-87263-871; PubMed=3037705;
MEDILIBE-87263-871; PubMed=3037705;
Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                 regulation of cytosolic calcium in a eukaryotic gene expression
                                                                                                                                                                                                                                                               MEDLINE=92101806; PubMed=1759615;
Lai J., Smith T.L., Mei L., Irkeda M., Fujiwara Y., Gomez J.,
Halonen M., Roeske W.R., Yamamura H.I.;
"The molecular properties of the MI muscarinic receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Muscarinic acetylcholine receptor M1.
CHRM1 OR CHRM-1.
     460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                        Adv. Exp. Med. Biol. 287:313-330(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M16406; AAA40660.1; -. EMBL; S73971; AAB20705.1; -.
                                                                                                                                                                                                                            Science 237:527-532(1987).
                                                                                              Rattus norvegicus (Rat).
        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
82
82
1121
1141
1164
1186
2209
3366
387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A94518; A29514.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=10116;
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TRANSMEM
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62 FLVGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LIIGTESMNLYTTYLLMGHWALGTLACDLWLALDYVASNASVMNLLLISFDRYFSVTRPL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 YILTITMLLEFLLPVISVAYFNVQIYWSLWKR-----RAL----SRCPSHAGFSTISSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IITFGTAMAAFYLPVTVMC----TLYWRIYRETENRARELAALOGSETPGKGGGSSSSSE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 AS-----GHLHRAGVACRT-----SNPGLKESAASRHSESPRRK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 RŚQPGAEGSPESPPĠRCCŔ---CĊŔAPRLLQAYSWKEEEEEDEĠSMEŚLTŚSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RTHMNSSITAFKVGSFWRSESA-----ALROREY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 SEVVIKMPMVDSBAQAPTKQPPKSSPNTVKRPTKKG---RDRGGKGQKPRGKBQLAKRKT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 AELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSF 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 NITVLAPGKGPWQVAPIGITTGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSLACAD
                                                                                                                                                                                                                                                                                                                                                  5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISD
                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                             90;
                                  CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (PROBABLE)

PROBABLE.

PROSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94339178; PubMed=8061048;
Lee P.H., Hodges P.K., Glickman F., Chang K.J.;
"Cloning and expression of a cDNA encoding bovine muscarinic
accerylcholine m3 receptor.";
                                                                                                                                                                                                                                                             20.0%; Score 410; DB 1; Length 460; 27.4%; Pred. No. 7.8e-21; ive 83; Mismatches 151; Indels
                                                                                                                                                     (POTENTIAL). (POTENTIAL). (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                        527573ED8FF7C317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Muscarinic acetylcholine receptor M3.
                                                                                                                                                     PHOSPHORYLATION
PHOSPHORYLATION
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| | ||::|::|
vnpmcyalcnkafrdtf-rlilicrw
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01-NOV-1995 (Rel. 32, Last seq
15-MAR-2004 (Rel. 43, Last anno
                                                                                                                                                                                                                          51368 MW;
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SEQUENCE OF 327-467 FROM N.A.
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                                                                                                                                                                                                                                                                                                               Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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12
178
428
451
455
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12
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428
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457
460 AA;
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TISSUE=Brain,
                                                                                                                                                                                                                                                                                          Similarity
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Caenorhabditis elegans.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                  246 SAASR-
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                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                     -!- FUNCTION: The muscarinic acetylcholine receptor mediates various cellular responses, including inhibition of adenylate cyclase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
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                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                           breakdown of phosphoinositides and modulation of potassium channels through the action of G proteins. Primary transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00001; /cm_1, ...
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP FI 1; 1.
PROSITE; PS50262; G_PROTEIN TRECEP_FI_2; 1.
POSTUBAPTIC membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.

67
EXTRACELLULAR (POTENTIAL).
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                              Sui A.-L., Chou W.-Y., Kao L.-S.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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EMBL; L27103; AAA30653.1; -.
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                                           PVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STTSSSASGHLHRAGVACRTSNPGLKE 245
                                                                                                                                                                                     357
                                                                                                                                                                                                                                                           GSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEEELGSVGLERKPSKLQTQQSMDDG 417
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                                                                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                 243 PVTIMTI----LYWRIYKETE-KRTKELAGLQASGTEAEAENFVHPTGSSRSCSSYELQQ
                                                                                                                                                                         298 QSMKRSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEBDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=20100976; PubMed=10635059;
HWang J.M., Chang D.-J., Kim U.S., Lee Y.-S., Park Y.-S., Kaang B.-K.,
Cho N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and functional characterization of a Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: The muscarinic acetylcholine receptor mediates various cellular responses, including inhibition of adenylate cyclase, breakdown of phosphoinositides and modulation of potassium channels through the action of G proteins. Primary transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  effect is PI turnover.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACM3_CAEEL STANDARD, PRT; 585 AA.
0907D5; QSXW31;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
acceylcholine receptor gar-3 (G-protein linked GAR-3 OR Y40H4A.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMurray A.A., Mortimore B.J.,
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Durbin R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     255 ---PRRKSSILVSLRTH---MNS----SITAFKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSFVNPFLYPLCHRRFQKAFWKIL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine receptor.";
Recept. Channels 6:415-424(1999).
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us-10-626-445-8.rsp

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TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 NISPPCTPMPTNFEDEEQTDAGASMRNGSARFRSRPSDTGKNNNSDTYTVLIELNDEGSR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RTHMNSSI-----TAFKVGSFWRSESAALRQR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 PSVRLSSCEPYLDEPISTRNRSKSDCNSEIDERRHSLLNKQSPFKNGRILKNFSSQERKS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 -VLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VMIVVIGAMFALVITSLGNLMVMVSFKIDKQLQIISNYFLFSLAVADIAIGVISIPMFTYY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 VPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 QMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG-----FVTEWYILTITMLLEFLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 VEDSVTPCTSSRNSKRKSWLRNCTGKSNSSSEDSSEAVAMNLDDTSLSSSHFALSGSRRR
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      / Match 19.9%; Score 408; DB 1; Length 585; Local Similarity 23.7%; Pred. No. 1.3e-20; nes 123; Conservative 83; Mismatches 160; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 585;
                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                    S (FOIENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  0770C89B756F71DC CRC64;
                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                    coupled receptor; Transmembrane;
                                                                                                                                                                                                               (POTENTIAL).
                                                                                                             Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_I 1; 1.

PROSITE; PS50262; G PROTEIN RECEP_FI 2; 1.

Receptor; G-protein coupled receptor; Tran
                                                                                                                                                                                                                                                                                  (POTENTIAL)
email to license@isb-sib.ch)
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                                         EMBL; Z81486; CAA22301.2; JOINED.
EMBL; Z81486; CAC42272.1; -
EMBL; AL034391; CAC42272.1; JOINED.
PIR; T20171; T20171.
                                                                             PIR; T20171; T20171.
WormPep; Y40H4A.1; CE27783.
InterPro; IPR000276; GPCR_Rhodpsn.
                     EMBL; AF139093; AAD48771.1; -. EMBL; AL034391; CAA22301.2; -.
                                                                                                                                                                                                                                                                                                                                                                                     66469 MW;
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585 AA;
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                                                                                                                                                                    Multîgene family.
DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The muscarinic acetylcholine receptor mediates various cellular responses, including inhibition of adenylate cyclase, breakdown of phosphoinositides and modulation of potassium channels through the action of G proteins. Primary transducing effect is PI turnover.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Puhl H.L. III, Ikeda S.R., Aronstam R.S.; aclones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90166521; PubMed-3272174;
Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
"Cloning and expression of the human and rat m5 muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Lens epithelium;
Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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MIM; 118496; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
540 CYINSTINPLCYALCNARFRHTYMRILKCKFKAERPTMNQ
                                                                                                                                                                                                                              ACMS HUMAN STANDARD; PRT; 532 AA. P08912; Q96RG7; 01-NOV-1988 (Rel. 09, Created) 01-UNV-1994 (Rel. 29, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Muscarinic acetylcholine receptor M5.
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TISSUE=Epidermal keratinocytes;
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Neuron 1:403-410(1988).
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EMBL, AAB08428; BAB9122.1; -.
EMBL, AF499919; AAM18942.1; -.
EMBL, AF38591; AAK68116.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 KIVAQMVAVWILAFLVNGPMILASDSW-----KNSTNTKDCEPGFVTEWYILTITMLLEF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 YIPVSVMTILYCRİYRETEKRTKDLADLQGSDSVTKAEKRRAHRALFRSCLRCPRPTLA 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290
GO; GO:0004981; F:muscarinic acetylcholine receptor activity; TAS. GO:0007213; P:acetyl choline receptor signaling, muscarin. .; TAS. GO; GO:0008283; P:cell proliferation; TAS. GO; GO:0007197; P:muscarinic acetyl choline receptor, adenyla. .; TAS. GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydro. .; TAS. InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RALSRCP---- 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.8%; Score 404.5; DB 1; Length 532;
24.6%; Pred. No. 2.1e-20;
Live 91; Mismatches 141; Indels 141; Gaps
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PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0262; G PROTEIN TRECEP F1 2; 1.

POST:Synaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.

Phosphorylation; Multigene family; G-protein coupled receptor.

29

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

BY SIMILARITY.
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PHOSPHORYLATION (POTENTIAL)
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EE846186F645DD9B CRC64;
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501 TFRKTF-KMLLLCRW 514
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Matches 122; Conservative
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Search completed: October 1, 2004, 10:11:50 Job time : 17 secs

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Query Match
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Q91x49 rattus norv
Q8653 canis famil
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Q9n2b1 gorilla gor
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Q8is43 drosophila
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Q8t3c1 caenorhabdi
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ALIGNMENTS

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DT Q1272
DT Q1272
DT Q1-DEC-2001 (TrEMBLrel. 19, Created)
DT O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
BE Histamine H4 receptor.
GN Mus musculus (Mouse)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PRINTS; PR00237; GFCRHDODPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 30 AA; 44469 MW; CC82B530D216C66 CRC64;
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iive 41; Mismatches 81;
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Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel. Histamine receptor H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
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Caralwasprague-Dawley;

Caralwasprague-Dawley;

Liu C., Wilson S., Kuei C., Lovenberg T.W.;

Liu C., Wilson S., Kuei C., Lovenberg T.W.;

Liu C., Wilson S., Kuei C., Lovenberg T.W.;

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                                                                                                                                                                   DFLVGLISIPLYIPHVLENWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV
                                                                                                                                                                                                                          SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
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                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                 Gaps
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               1; Indels
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PROSITE; PS50262; G-PROTEIN_RECEP_F2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
G-protein S1 PA; 44023 MW; C70TBA6E39CFED41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.2%; Score 1745; DB 11;
84.9%; Pred. No. 3.6e-144;
iive 17; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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                      Conservative
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332; Conserv
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ITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRT
                        SNPGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELL
                                                                                                                     RGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPF
                                                                                                                                                                                                                              298 RARKLARSLAILLGVFAICWAPYSLLTITRSVYPTNPFPSTAVYKFAFWLOWFNSCVNPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 SLLEFLIPILLVAYFSAHIYWSLWKREKLSRCLSHPVLPSDSSSSDHGHSCRQDPDSRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cavia porcellus (vainea pig).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleost
Mammalia: Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 7e-100;
43; Mismatches 100; Indels
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PRINTS; PR01726; HISTAMINEH4R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 389 AA; 44511 MW; 51AF32FD6F1C3E4F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                 LYPLCHRRFOKAFWKILCVTKWPALSQNQSVSS 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-UTN-2003 (TrEMBLrel.
Histamine H4 receptor.
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                                                                                                                                                                                              241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                                                                                                                                                                                              SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                      MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
                                                                                                                                      RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                                                                                                      59 ISDFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ISDFFVGVISIPLYIPHTLFYWKLEDNICAFWLIIDYLLCTASVYNIVLISFDRYQSVSN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Sus.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor: Receptor; Transmembrane.
SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig)."
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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65.9%; Pred. No. 2.7e-106;
ive 33; Mismatches 96;
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PLCHKRFOKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                                                                                                                                                                                                                                                                                                                                          PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS
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PRINTS; PR01726; HISTAMINEH4R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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01-MAR-2002
            121
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Matches
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78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
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                                                                                           APYCLETIVLSTYPRIERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILCVT 378
                                                                                                                              18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFINLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAYENVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRH
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Gaps
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Weiner D.M.;

Wolecular Cloning and Characterization of Functionally Distinct

Twolecular Cloning and Characterization of Functionally Distinct

I submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

BMBL; AF321911; AML71912.1;

GO; GO:0016021; Cintegral to membrane; IEA.

RO; GO:0004872; Fintegral to membrane; IEA.

RO; GO:0004872; Fintegral receptor activity; IEA.

RO; GO:001584; Finteramine receptor activity; IEA.

RO; GO:001584; Firthodopsin-like receptor activity; IEA.

RO; GO:0001584; Firthodopsin coupled receptor protein signalin...;

RO; GO:007186; P:G-protein coupled receptor protein signalin...;

RINEDRO; IPR000296; HI-receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Hippocampus;
Wellendorph P., Goodman M.W., Burstein B.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AA; 40609 MW; D78B32042464CB35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AA
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PRINTS; PR01237; GPCRRHODOPSN.

PRINTS; PR01471; HISTAMINEH3R.

PROSTITS; PS01237; G PROTEIN RECEP F1 1; 1.

PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                             K 379
                                                                                                                                                                                                                                                                                           K 431
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                                             297
                                                                                                           GRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 VAVWILLAFLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 LLVWVLAFLLYGPAIL---SWBYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 VIFFNLSIYLNIQRRIRLDGAREAGGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILVSLRT
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         298 ARKLAKSLAILLAAFAICWAPYSLTTVIYSFFPERNLTKSTWYHTAFWLQWFNSFVNPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. YAO B.B., Sharma R., Cassar S., Esbenshade T.A., Hancock A.A.; Yao B.B., Sharmacological Characterization of the Monkey Histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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EMBL, AV231164; AAO63757.1; -...

EMBL, AV231164; AAO63757.1; -...

EMBL, AV231164; AAO63757.1; -...

EMBL, AV231164; AAO63757.1; -...

GO; GO:0016021; F:integral to membrane; IEA.

GO; GO:0004872; F:integral activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; F:rhodopsin-like receptor protein signalin.

InterPro; IPR00276; GRCR Rhodopsn.

InterPro; IPR00276; GRCR Rhodopsn.

InterPro; IPR003809; H3_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
35.1%; Score 718.5; DB 6;
Best Local Similarity 38.7%; Pred. No. 2e-54;
Matches 163; Conservative 52; Mismatches 121;
                                                                                                                                                                                                                                          YPLCHRRFOKAFWKILCVTKWPALSQNQSVSS 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
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PRINTS; PR00237; GFCRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
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(TrEMBLrel. 24, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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01-OCT-2003
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SEQUENCE
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80
311 LSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKA 370
                      :||:|||||||||::
284 VSIFGLCWAPYTLLMIIRAACHGHCVP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 SESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELL-RGRKLARSLAIL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 VAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYLLTITMLLEFLLPVIS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ||:||||: || || || ||:|
157 LLVMVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 VAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GCW-----GCWQKGHGEAMPLHRKVAKSLAVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isoforms of the Human Histamine H3 Receptor.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF321913; AAL71914.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004969; F:histamine receptor activity; IEA.
GO; GO:0004819; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:Crotein coupled receptor signalin..
InterPro; IFR000276; GPCR_Rhodpsn.
InterPro; IFR0003989; H3_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Weiner D.M., "Molecular Cloning and Characterization of Functionally Distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.5%; Score 665.5; DB 4; Length 373; 40.1%; Pred. No. 6.9e-50; tive 46; Mismatches 114; Indels 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA; 41570 MW; FAE9DFC5C3AF4DE9 CRC64;
                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Histamine H3 receptor isoform 4.
                                                                                                                                                                                        373 AA.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 148; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                  371 FWKILCVTK 379
                                                                                                 FTKLLCPQK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
                                                                                                   343
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F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular Cloning and Characterization of Functionally Distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, #7821912, AAL71913.1;

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0004959; F:histamine receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; P:G-Protein coupled receptor protein signalin.

InterPro; IPR000276; GPCR_Rhodopsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;
                                                                                                                                                                                                                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Histamine H3 receptor isoform 3.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Histamine H3 receptor isoform 6.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                   Created)
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214 VTFFNLSIYLNIORRTRL 231
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20,
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Matches 100; Conservative
                                                                                                                                                                                                                     PRELIMINARY;
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371 FWKILCVTK 379
                                                             343 FIKLLCPOK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                        (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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SEQUENCE
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL, AY072062; AAL67913.1;
-GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                           Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi K.
                                                                                                                                                                                                                                                                         and Characterization of Functionally Distinct
                                                                                                                                                                                                                                                                         "Molecular Cloning and Characterization of Functionally Distinct Isoforms of the Human Histamine H3 Receptor.";

Isoforms of the Human Histamine H3 Receptor.";

Neuropharmacology 0:0-0 (2002).

EMBL; AF346904; AAM43829.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004992; F:nistamine receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin...

InterPro; IPR0003980; H3_receptor.
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Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.0%; Score 492.5; DB 4; Length 50.5%; Pred. No. 7.1e-35; ive 30; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B7496F7D1D2A206B CRC64;
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Last annotation update)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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PRINTS, PR00237, GPCRRHODOPSN.
PRINTS, PR01471, HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AA; 34242 MW;
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"Cloning Cholinergic Receptors in Human Keratinocytes.";
"Cloning Cholinergic Receptors in Human Keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DBB databases.
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF385597; AAK68112.1; --
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
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PROSITE; PS00237; GFCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
G-PROSITE; PS50262; G-ROTEIN RECEP F1 2; 1.
G-PROSITE; PS50263; G-ROTEIN RECEP F1 2; 1.
G-PROSITE; PS5036 MS 25938 MW; 22CGD68BFADICDAB CRC6
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Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                       Pfam; PF00001; 7tm_1; 1.
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NCBI_TaxID=10141;
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                                                                                                                                        Query Match
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Nature 420:563-573 (2002).
EMBL; AK081248; BAC38175.1; -.
                                                                                                                                                                                                          5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISD
                                                                                                                                                                                                                                                                                                                                                                175 YILTITMILEFILPVISVAYFNVQIYWSLWKR-----RAL----SRCPSHAGFSTTSSS
                                                                                                                                                                                                                                                                                                                                                                                  SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                        20.2%; Score 413; DB 4; Length 454; 27.4%; Pred. No. 9.9e-28; Ive 84; Mismatches 150; Indels
                                                                                                                                68D02A29898C8D92 CRC64;
                                                                          PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last seq.
01-OCT-2003 (TrEMBLrel. 25, Last annomancarinic acetylcholine receptor MI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Striatum; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                 454 AA; 50748 MW;
                                                                                                                                                                      Best Local Similarity 27.4%;
Matches 122; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 SSILVSL-----
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                                                                                                                                                                    Similarity
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01-MAR-2003
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62 FLVGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
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                                                                                                                                                                                                                                                                                       NSTGILPPAAQVPLAFI----MSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 IITFGTAMAAFYLPVTVMC----TLYWRIYRETENRARELAALQGSETPGKGGGSSSSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 SEVVIKMPMVDPEAQAPTKQPPKSSPNTVKRPTKKG---RDRGGKGQKPRGKEQLAKRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 AELLRGRKLARSLALLLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Five subtypes of muscarinic receptors are expressed in gastric smooth
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscles of guinea pig.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL, AY072066), AAL67911.1,
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPRO0027; GPCR.Rhodpsn.
PRINTS; PRO0021; Tum 1; 1.
PROSITE; PRO00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS500237; GPROTEIN RECEP F1 2; 1.
SEQUENCE 460 AA; 51378 WW; 2PEA93DE8FF4F325 CRC64;
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                                                                                                                                                                                                               Length 460;
                                                                                                                                                                                                                                ; Pred. No. 1.8e-27;
83; Mismatches 151; Indels
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Last annotation update)
                                                                                                                                                                                                               DB 11;
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                                                                                                                                                                                                             20.0%; Score 410;
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                                                                                                                                                                                                                             Local Similarity 27.4
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                                            Receptor.
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ISSUE-Testis:
Strausberg R.;
Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2002), --
EMBL; BC041805; AAH41805.1; --
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004812; F:receptor activity; IEA.
GO, GO:0001584; F:receptor activity; IEA.
GO; GO:0007186; P:d-protein outpled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                   VAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYILTITMLLEFLL
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                                                                                                                                                     LAFLMSSFAFAIMVGNAVVILLAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                                              -----RRALSRCPSHAGFSTT------SSSASGHLHRAGVACRTSN----
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
GO; GO:0007186; P:G-protein coupled receptor protein signalin. InterPro; IPR00276; GPCR_Rhodpsn.
Pffan; PF00001, 7tm_1; 1.
PRO037; GFCRRHODPSN.
PROSITE; PS00237; GFCRRHODPSN.
PROSITE; PS00262; GFROTEIN_RECEP_F1_1; 1.
G-protein coupled receptor; Receptor; Transmembrane.
G-protein coupled receptor; 39760B2893BD7BDA CRC64;
                                                                                                                                  168;
                                                                                                        20.0%; Score 410; DB 11; Length 587; 24.7%; Pred. No. 2.5e-27; ive 90; Mismatches 123; Indels 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Cholinergic receptor, muscarinic 5.
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                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                  131 KIVAQMVAVWILAFLVNGPMILASDSW-----KNSTNTKDCEPGFVTEWYILTITMLLEF 185
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                                                                                                                                                                                                                       16 VPLAFLMSSFAFALMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPH
                                                                                                                                                                                                                                                                                                                                                                                                                               ------RALSRCP----
                                                                                                                                                                  Gapa
                                                                                                                                                                141;
                                                                                                                           19.8%; Score 406.5; DB 4; Length 25.1%; Pred. No. 4.4e-27; tive 89; Mismatches 141; Indels
                                                                                      532 AA; 60085 MW; 6674707A1B493C67 CRC64;
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHOODESN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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Matches 124;
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Geneseq_29Jan04:*
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 geneseqp2001s:* geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database

Post-processing: Listing first 45 summaries

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AamS0566 Rat hista AamS0566 Rat hista Aag80931 Human Gp Aag83749 Human Gp Aac5415 Human Gp Aac5415 Human Gp Aac71297 Human Gp Aab71297 Human GpC Aag64477 Human GpC Aag64477 Human GpC Aag646477 Human GpC Aag646477 Human GpC Aab73622 Human GpC Aab73622 Human GpC Aab736245 Human GpC Aab73629 Human his Aab78276 Amino aci AamS0569 Human his AamS0569 Human his G-p G-p his H 4 G G д aci Human Human Human Amino Human Description Aagg0931 Abg93749 Aae36415 Aab02831 Aay71297 Aab62447 Aab64477 Aam53050 Abb78629 Abb78629 Abb78629 Abb78629 Aag66023 Hau74906 Aau74906 Abg71960 Abb92265 Habb81727 Aac36417 Aac36416 Aam53052 Ham53053 Ha SUMMARIES AAM50566 AAM50567 AAG80931 AAE36415 AAB02831 AAY71297 AAB62445 AAG64477 AAB73622 AAM53050 ABP98629 AAE36416 AAM53052 AAM53053 ABB78276 AAM50564 AAG66023 AAU74906 ABP81727 AAE36417 ABG93749 Length DB Query Match Score Result

Human

Aae23411 Human G-p Abg28404 Novel hum Abr25788 Movel hum	Human	Aag67840 Rat mACHR Aag67840 Rat mACHR Abq76408 Himan mis			Human Human		Aabazazari Human his Aag65581 Human his Aag65580 Kuman his	Aao29528 Human H3
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AAMSOS65 standard; protein; 391 AA. AAMSOS65 standard; protein; 391 AA. AAMSOS65; XX AAMSOS65; XX AAMSOS65; XX AAMSOS65; Mouse histamine H4 receptor. XX W Histanine H4 receptor. XX W Histanine H4 receptor. XX A martinflammatory; cardiant; circulatory; antidiabetic; laxative; XX XX XX XX XX XX XX XX XX
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for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                                                                                                                                                                                                                                                            SYRAQHIGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
                                                                                                                                                                        Gaps
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                                                                                                                                   DB 5; Length 391;
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                                                                                                                           96.9%; Scor.
100.0%; Pred. No. c,
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N-PSDB; AAI70982.
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                                                                                                                                                          Similarity
                                                                                                    Sequence 391 AA;
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Best Local Simil
Matches 379; C
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The present sequence is that of a rat histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA subtype, as predicted from a cDNA clone isolated from a spleen cDNA subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (mee AALT0980-83) and polypeptides (see AAMS0564-67). The nucleic acids have been expressed in polypeptides (see AAMS0564-67). The nucleic acids have been expressed in pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of thistamine H4 receptor activity. Recombinant protein is useful for identifying medulators of the histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, candidovascular and carebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding
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beneficial to elevate mammalian histamine H4 receptor activity.
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Pred. No. 1.5e-24;
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100.0%; Pred. No. 1...
1... 0; Mismatches
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                                                                      English
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                                                                         Claim 13; Fig 6A; 92pp;
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es 33; Conserv
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recombinant host cells that produce active recombinant protein. The histamine Hy receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine Hy receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; neuroprotective.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
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100.0%; Pred. No. 1.6e-2;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        AAG80931 standard; protein; 73 AA.
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99US-0166071P.
99US-0166678P.
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2000US-0185554P.
2000US-0186530P.
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2000US-0184129P.
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                Conservative
                                                                                                                                                                    Query Match
Best Local Similarity
....hes 32; Conserve
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                                                                                                                                                       Sequence 389 AA;
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28-FEB-2000;
02-MAR-2000;
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28-DEC-1999;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2001
                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                    AAG80931;
                                                                                                                                                                                                                                                                                                              RESULT 4
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The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
31-38, 40, 41, 53-60) and their coding sequences. The present sequence is

consuch G protein-coupled receptor. GPCRs are also known as seven

consuch G protein-coupled receptor. GPCRs are also known as seven

coding sequences are useful for screening a human to diagnose a disorder

coding sequences are useful for screening a human to diagnose a disorder

coding sequences are useful for identifying compounds useful for

creating schizophrenia. Detection of nGPCRx in a sample is useful as a

contagnostic tool for diseases or disorders e.g. thyroid disorders, renal

configuration deficit and cardiovascular diseases, proliferative disorders and

chormonal disorders. Modulators of nGPCRx activity have the utility for

treating neurological disorders in nocluding schizophrenia, ADHD/ADD

conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

disorders, cancers all alsorders all and seconds and inflammatory

conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

disorders cancers and respirators and inflammatory

conditions (e.g. crohn's hours) as asthma, and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                           encoding polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR; nG protein coupled receptor; communication; serpentine structure; seven transmembrane receptor; 7TW; mental disorder; diagnosis; genetic predisposition; brain; immune response; gene therapy; anxiety disorder; depression; bipolar disorder; schizophrenia; Huntington's disease; dyskinesia; manic depression; stroke; Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4%; Score 21; DB 4; Length 73;
100.0%; Pred. No. 5.1e-13;
tive 0; Mismatches 0; Indels
                                    New G protein-coupled receptor (nGPCR-x) and its encoduseful for diagnosing and treating e.g. schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human G protein-coupled receptor protein, beGPCR-seg4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases e.g. inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood LS;
                                                                                            Claim 37; Page 77; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG93749 standard; protein; 73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vogeli G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2001; 2001WO-US004641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2001; 2001WO-US004641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parodi LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
N-PSDB; AAH50971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200264789-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
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WPI; 2002-674879/72

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AAE36415 standard; protein; 357 AA
                                                                                                                                                                                                                    93 TDYLLCTASVYNIVLISYDRY 113
                                     Example 1; Page 72; 244pp; English.
                                                                                                                                                                         referred to as beGPCRs) proteins
                                                                                                                                                                                                                           31 TDYLLCTASVYNIVLISYDRY
                                                                                                                                                                                                                                                                                                                                                                              31-AUG-2001; 2001US-0316762P.
13-NOV-2001; 2001US-0332697P.
                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2002; 2002WO-US027891.
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC.
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                              WO2003020907-A2.
N-PSDB; ABS70204
                                                                                                                                                                                     Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                               07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                         13-MAR-2003
                                                                                                                                                                                                                                                                     AAE36415;
                                                                                                                                                                                                                                                RESULT 6
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Novel splice variants of human H4 histamine receptor, H4b and H4c, useful for identifying agonists or antagonists of the receptor which are useful for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                                                                               The invention relates to splice variants of human H4 histamine receptor, H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4c is useful for recating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, or psoriasis. The present sequence is human H4c protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%; Score 21; DB 6; Length 357; 100.0%; Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                   Claim 21; Page 50-51; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB02831 standard; protein; 390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 TDYLLCTASVXNIVLISYDRY
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98US-0108023P.
98US-011005013P.
99US-0120416P.
99US-0121852P.
99US-0123944P.
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99US-0123951P.
99US-0136436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                  Gallagher MJ, Yates SL;
                                                              2003-290186/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 357 AA;
                                                                                     N-PSDB; AAD55124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200022131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-1998;
27-NOV-1998;
16-FEB-1999;
26-FEB-1999;
12-MAR-1999;
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12-MAR-1999;
12-MAR-1999;
12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                         The invention discloses an isolated human polypeptide, and encoding nucleic acid, for a G protein-coupled receptor (GPCR), particularly the nucleic acid, for a G protein-coupled receptor (GPCR), particularly the communication between cells and their environment and are characterised communication between cells and their environment and are characterised by a serpentine structure that passes through the cell membrane seven times, hence the receptors are sometimes called seven transmembrane receptors (TMM). The polypucleotides and polypeptides are useful for identifying an nGPCR allalic variant that correlates with a custom polypeptide and/or modulates its biological activity, for screening a human subject to diagnose a disorder, or a genetic predisposition to a disorder, affecting the brain or a genetic disposition to the disorder. Cor identifying a compound useful for the treatment of a mental disorder and for identifying a compound useful as a modulator of binding between GPCR-14 and a binding partner of nGPCR-14. The polypeptide is also useful for inducing an immune response in a mammal. The nucleic acid or polypeptide is particularly useful, using gene therapy, for treating e.g. mixiety disorders, depression, bipolar disorder, schizophrenia, considered in a mammal. The nucleic acid or anxiety disorders, disease, dyskinesias, manic depression, stroke, Parkinson's be used for treating diabetes, inflammation or wounds. The sequences or presented in ABG931795 and ABG931795 are the nGPCR (also presented in ABG931795 and ABG931795 are the nGPCR (also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, H4; histamine receptor; inflammatory bowel disease; psoriasis; atopic dermatitis; stroke; myocardial infarction; migraine; allergy; chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy; rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective; asthma; receptor; variant.
                                       New nucleic acids and polypeptides of the nG protein-coupled receptor, useful for treating or diagnosing a mental disorder or a disorder affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.4%; Score 21; DB 5; Length 73;
100.0%; Pred. No. 5.1e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human H4 receptor splice variant (H4c) protein.
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99US-0137127P. 99US-0137131P. 99US-0137567P. 99US-0136437P.

28-MAY-1999 28-MAY-1999 28-MAY-1999 28-MAY-1999

L2-MAR-1999

99US-0141448P

27-AUG-1999;

28-MAY-1999 29-JUN-1999

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Gaps

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0; Indels

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Homo sapiens
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Matches
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             ਨੇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46116 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                          Non-endogenous, human G protein-coupled receptors for screening receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening; transmembrane receptor; signal cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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100.0%; Pred. No. 2.6e-12;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 inverse or partial agonists useful as therapeutic agents.
                                                                                                                                                                                                                                                                                     Chen R,
                                                                                                                                                                                                                                                                               Lehmann-Bruinsma K, Chalmers DT, ciaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human orphan G protein-coupled receptor hRUP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 89-90; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY71297 standard; protein; 390 AA
990S-0155524P
990S-015653F
990S-0156634P
990S-0156634P
990S-015653P
990S-0157280P
990S-0157281P
990S-0157281P
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99US-0120416P.
99US-0121852P.
99US-0123946P.
99US-0123949P.
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99US-00417044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
nes 21; Conservative
                                                                                                                                                                                                                                          (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                   WPI; 2000-317986/27.
                                                                                                                                                                                                                                                                                                Liaw CW,
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA46023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200031258-A2
                                                                                         01-OCT-1999;
                                                                                                                                                                  01-OCT-1999;
12-OCT-1999;
                                                                                                                                                                                                       12-OCT-1999;
                                                                           29-SEP-1999;
                                                                                                                              01-0CT-1999;
                                      29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
                                                        29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999;
12-MAR-1999;
12-MAR-1999;
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                                                                                                                                                                                                                                                                                 Behan DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71297;
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                                                                                                                                                                                                                                                                                                  Gore M,
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Matches
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The present amino acid sequence is the hRUP7, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned by RT-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation in expression analysis to provide information about their function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic; antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human; osteopathic; neuroprotective; nootropic; dermatological; gynecological; signal transduction.
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Pred. No. 2.6e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Page 60-61; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 TDYLLCTASVYNIVLISYDRY 113
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                                                                       99US-0136567P.
99US-0137127P.
99US-0141448P.
99US-0156555P.
99US-0156633P.
                                                                                                                                                                                                                                              99US-0156653P,
99US-0157280P,
99US-0157281P.
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99US-0157293P.
99US-0157294P.
99US-00416760.
                         99US-0136437P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-400068/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARENA
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
                                                                                                                                               29-JUN-1999;
29-SEP-1999;
29-SEP-1999;
29-SEP-1999;
                                                                          28-MAY-1999
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01-OCT-1999;
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Ohta M;

EP1096009-A1. 02-MAY-2001

Peter B,

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The present sequence is that of the human G protein-coupled receptor protein BG26, which shows significant homology with histamine H3, with activity of binding to histamine and capable of changing intracellular cAMP concentration in response to its simulus. The protein is applicable as a tool in screening ligands or drug candidates for regulating signal transduction from such protein and treating diseases associated with its
                                                                                                                                                                                                                                                                           G protein-coupled receptor protein BG26, with activity of binding to histamine and capable of changing intracellular cAMP concentration in response to its stimulus, applicable as tool in screening ligands or drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; guanosine triphosphate-binding protein-coupled receptor; GPRV53; intracellular calcium ion regulation; histamine receptor; leukocyte.
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Pred. No. 2.6e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 41-44; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM51410 standard; protein; 390 AA.
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                                                                                                                                                                                Tanaka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 TDYLLCTASVYNIVLISYDRY
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2000JP-00163147.
2000JP-00223870.
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                                                        20-DEC-2000; 2000WO-JP009038.
                                                                                               99JP-00361687
                                                                                                                                           (BANY ) BANYU PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; AAI66009.
                                                                                                                                                                                      Nakamura
                                                                                                                                                                                                                             WPI; 2001-441675/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                               N-PSDB; AAH47911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 390 AA;
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Sugiyama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2000;
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                                                                                                   20-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abnormality
                   28-JUN-2001
                                                                                                                                                                                      Itadani H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
CO 113, encoded by CDNA of NCIMB 41073. The PFI-013 protein can be expressed
CO 125, encoded by CDNA of NCIMB 41073. The PFI-013 protein can be expressed
CO 25 are useful in the manufacture of a medicament for treating allergic
CO constituting extrinist asthma, immunological disorders, such as
intrinsic asthma, vascultic granulomatous disease, interstitial and
COCDD), infectious, inflammatory disease, such as inflammatory bowel
COCDD), infectious, inflammatory disease, such as inflammatory bowel
COCDD), infectious, inflammatory disease, such as inflammatory bowel
COCDD, infectious, inflammatory disease, such as inflammatory bowel
COC useful for treating obseity, diabetes, metabolic, neurological disease,
COC useful for treating obseity, diabetes, reproduction and sexual medicine,
inflammation, cancer, tissue repair, dermatology, photoageing, skin
COC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,
callergy and respiratory disease, sensory organ disorders, sleep disorders
and hair loss. The PFI-013 protein and nucleic acid are useful in the
COC diagnosis and treatment of the above conditions and also for screening
COC diagnosis and treatment of the above conditions and also for screening
conditions and also for enrichment of transduction. The antibodies are also useful for enrichment of transduction, the muthodies are also useful for enrichment of electring the
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                                                                                                                                                                                                                                                                                                                                                                           New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G protein-coupled receptor protein BG26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Scc.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 44; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein in biological samples
                                                                                                                                                     29-OCT-1999; 99GB-00025641.
20-APR-2000; 2000GB-00009973.
                                                                                                                 24-OCT-2000; 2000EP-00309364.
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                                                                                                                                                                                                                                                                                 O'reilly MA;
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Best Local Similarity
                                                                                                                                                                                                                     (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF83203.
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0

Gaps

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Length 390;

Suwa M;

Yoshida K,

Morikawa N,

WO200146414-A1

AAG64477;

RESULT 10 AAG64477

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Matches

7

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PREVEST. GERVES is a new type of histamine receptor which is preferentially expressed in peripheral leukocytes and on stimulation with histamine causes a change in intracellular calcium ion concentration. GERVES is useful in the identification of antagonists and agonists of histamine binding to GERVES and disorders. Also, since the receptor protein is preferentially expressed in tissues (especially in peripheral leukocytes) other than those associated with the known histamine receptor types H1-H3 it is useful in the investigation of the role of histamine and its receptors in the tissues in which it is expressed
                           cation of agonists and antagonists as drugs active in histamine-
                                                                                                                                        The invention relates to human G-protein coupled histamine receptor
  Gene encoding a G-protein coupled histamine receptor protein for
                                                                                          Claim 1; Page 42-43; 51pp; Japanese.
                                             related disorders.
                           dentifi
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Sequence 390 AA;

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0
                                  Gaps
                                 ;
0
5.4%; Score 21; DB 4; Length 390; 100.0%; Pred. No. 2.6e-12; tive 0; Mismatches 0; Indels
                            21; Conservative
              Local Similarity
 Query Match
                          Matches
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AAB73622 standard; protein; 390 AA. RESULT 12 AAB73622 g

(first entry) 10-AUG-2001 AAB73622;

Human G protein-coupled receptor AXOR35.

AXOR35; human, G protein-coupled receptor; 7TM receptor; histamine H3 receptor homologue; infection; viral; bacterial; fungal; protozon; H1V-1; H1V-2; pain; cancer; diabetes; obesity; anorexia; bullimia; osteoporosis; asthmia; allergy; urinary retention; acute heart failure; hypotemsion; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delirium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; diles de la Tourette's syndrome; lymphocyte; macrophage; eosinophi; function modulation; lymphocyte; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery.

Homo sapiens.

WO200133221-A1.

10-MAY-2001

26-OCT-2000; 2000WO-US029461.

02-NOV-1999; 99US-00431898. 03-FEB-2000; 2000US-00497790.

(SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC.

Graybill TL, Fitzgerald LR, Michalovich D, Morrow DM, Bergsma DJ, Aubart KM,

WPI; 2001-316464/33. N-PSDB; AAH24007.

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the invention relates to the numbal of protein-coupled receptor AKOR35 cand variants in the invention relates to the numbal of protein-coupled receptors. AKOR35 has and variants. Like all G protein-coupled receptors, AKOR35 has card and variants. Like all G protein-coupled receptors, AKOR35 has composed in signal transduction. AKOR35 has homology and structural similarity with G protein-coupled receptors such as the human histeranian H3 receptor. The invention also relates to recombinant expression of AKOR35, and to an AKOR35-specific antibody. AKOR35 proteins and nucleorides may be used to treat a wide variety of disorders including bacterial fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertension; allereis including bacterial infarction; stroke; ulcers; migraine; vomiting; chapters; obesity; anorexis, bulimia; osteoporosis; asthma; allereis; companied depression, depression, depression, stroke; ulcers; migraine; vomiting; chapters; obesity; anorexis, bulimia; osteoporosis; asthma; allereis; comition; and neurological disorders such as anxiety, schizophrenia, pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; chapteris; myocardial infarction; stroke; ulcers; migraine; vomiting; completed and neurological disorders such as anxiety; schizophrenia, completed and neurological disorders and services and surface and services, and AKOR35 proteins, and dyskinesis, and AKOR35 proteins, mucleotides and untibodies are useful for treating asthma, and inhibiting or promoting to articolate architecture and completed and antibodies are also constituted and completed and antibodies are also consetulated to a the detection of abnormal levels of protein or manal against the detection of mutations in the corresponding gene. AKOR35 proteins are also useful for inducing an immunological response in a manal against the above diseases, and for producing transgenic animal submit or variance and useful so trading are also useful for producing are us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                        treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.
                                                                                                                                                           the invention relates to the human G protein-coupled receptor AXOR35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurologic
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100.0%; Pred. No. 2.6e-12;
Live 0; Mismatches 0;
                                                                                                      Claim 1; Page 50-51; 54pp; English.
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93 TDYLLCTASVYNIVLISYDRY 113

AAM53050

AAM53050 standard; protein; 390 AA. AAM53050;

26-MAR-2002 (first entry)

Human G protein-coupled receptor nGPCR-2067.

Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor; signal transduction; mental disorder; central nervous system disease; metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder; psychotic disorder; Huntington's disease; schizophrenia; migraine; depression; anxiety; bipolar disorder; dementia; Alzheimer's disease; Parkinson's disease; prollferative disorder; cancer; psoriasis; benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia; thyroid disorder; cardiovascular disease; hypotension; hypertension; thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis; inflammatory conditions; autoimmune disorder; rheumatoid arthritis;

; 0

Lind P, Domain Domain Domain Domain Domain Domain Domain Key

This sequence represents a novel human G protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCR8, nGPCR-2067 has 7 putative cransmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising involution also relates to expression vectors and host cells comprising concleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-2067 acids in cells and specific for nGPCR-2067, to drug screening methods that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067 and species homologues and may also used in genetic mapping. The invention also discloses the use of nGPCR-2067 nucleic acids in screening for a predisposition to nGPCR-2067-associated hereditary mental consorters, or for the diagnosis of these disorders. nGPCR-2067 nucleic acids may additionally be used to generate transgenic animals, including consorters, and may also be used in the design of antisense molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067, and nGPCR-2067 modulators may be used to treat a wide variety of medical conditions, particularly mental disorders, central nervous system conditions, particularly mental disorders, enciral nervous system conditions, particularly mill solved to reat a wide variety of medical contitions, particularly HIV-2 infections, pain, central convirs, and netabolic diseases because that may be treated included viral infections, particularly HIV-2 infections, pain, central nervous system, neurological and psychotic disorders such as Hutingfon's disease, and metabolic disease, and parkinson's disease; proliferative dementia, Alzheimer's disease, and Parkinson's disease; proliferative dementia, hyroid disorders such as dancers, benign prostatic hypertophy, and anorexia; thyroid disorders, cardiovascular diseases such as hypotension, anorexia; thyroid disorders, cardiovascular diseases such as hypotension, anorexia; thyroid disorders; cardiovascular diseases such as hypotension, anorexia; hypotensio New polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encodes the novel G protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067). hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant; antiatherosclerotic; neuroleptic; antimigraine; antiparkinsonian; tranquiliser; antidepressant; neuroprotective; anticonvulsant; antifflammatory; antirheumatic; antiathritic; antipsoriatic; gene therapy; receptor. /label= Transmembrane_domain_5 305. .326 /label= Transmembrane_domain_6 342. .360 /label= Transmembrane_domain_7 19. .41
/label= Transmembrane domain_1 /label= Transmembrane_domain_2 /label= Transmembrane_domain_3 128. .146 /label= Transmembrane_domain_4 Wood LS; Location/Qualifiers Claim 31; Page 63; 100pp; English Vogeli G, (PHAA) PHARMACIA & UPJOHN CO 08-MAY-2001; 2001WO-US014750. 08-MAY-2000; 2000US-0203108P. .110 Sejlitz T, 2002-062240/08. N-PSDB; ABA02496 WO200185793-A2 Homo sapiens 15-NOV-2001.

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This sequence represents the amino acid sequence of a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-cowpled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromatography, in immunoassay of histamine receptor, to identify CDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                   anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke anti-migraine; cardiant; anti-rheumatic; anti-arthritic; antipsoriatic; neuroprotective; inflammation; asthma; allergy; atopic dermatitis; myocardial infarction; migraine; chronic obstructive pulmonary disease; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid encoding antigenic part of human histamine receptor.
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               rheumatoid arthritis); hormonal disorders; and renal failure
                                                                                                                                                                                                                                                                                                                                                                                         human; histamine receptor; chromosome 18; anti-inflammatory;
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                                                                             Length 390;
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                                                                                                2.6e-12;
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                                                                                              100.0%; Pred. No. 2.6
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                                                                                                                                                                                                                                                            ABP98629 standard; protein; 390 AA
                                                                                                                                             93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                   Human histamine receptor SP9144.
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Best Local Similarity
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Them 21; Conservative
                                                                                                                                                                                                                                                                                                                            13-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis; receptor.
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Novel mammalian histamine receptor polypeptide useful for identifying agonist or antagonist for treating diseases such as inflammation, asthma, stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
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                                                                                                                                                                                                                                                                        Human; histamine receptor; receptor; inflammation; asthma; allergy; atopic dermatitis; stroke; myocardial infection; migraine; chronic obstructive pulmonary disease; COPD; rrhumatoid arthritis; multiple sclerosis; inflammatory bowel disease; psoriasis; inflammatory bowel disease; psoriasis; inflammatory pathway; cellular growth rate;
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                    Indels
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                   0
 Pred. No. 2.6e-12;
                                                                                                                                                                                                                                             Amino acid sequence of human histamine receptor.
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                   0; Mismatches
                                               113
                                                                 93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                    ABB78276 standard; protein; 390 AA.
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                                              93 TDYLLCTASVYNIVLISYDRY
   100.08;
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                 21; Conservative
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HEDRICK J A.
LAZ T M.
MONSMA F J.
MORSE K L.
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Best Local Similarity
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WANG S.
                                                                                                                                                                                                                                                                                                                                                        hormone secretion.
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                                                                                                                                                                                  ABB78276;
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(MORS/)
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5.4%; Score 21; DB 5; Length 390; 100.0%; Pred. No. 2.6e-12;

Query Match Best Local Similarity

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Gaps
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OM protein - protein search, using sw model

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October 1, 2004, 10:24:15; Search time 32 Seconds (without alignments) 630.805 Million cell updates/sec

391 1 MSESNSTGILPPAAQVPLAF......WKILGVTKWPALSQNQSVSS 391 US-10-626-445-8 Title: Perfect score:

Gapop 60.0 , Gapext 60.0 OLIGO Scoring table:

Sequence:

389414 segs, 51625971 residues Searched:

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Word size :

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Issued Patents AA: Database :

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	qi		US-09-414-010-2	US-09-812-216-2	US-08-985-090-8	US-09-165-543-8	US-09-165-543-15	US-09-524-162-2	US-08-985-090-2	US-09-165-543-2	US-09-165-543-5	US-09-167-354-7	US-09-642-855-7	US-09-642-514-7	US-08-985-090-5	US-09-165-543-32	US-08-833-226-2	US-09-107-532A-4457	US-08-985-090-9	US-08-985-090-15	US-09-165-543-9	US-09-165-543-16	US-09-165-543-35	US-09-177-249-243	US-09-621-976-5298	US-09-087-232A-18	US-09-489-039A-14289	US-09-087-232A-15	US-08-466-886-32
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de	Query		5.4	5.4	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.3	2.3	2.3	2.0	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8
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US-08-469-617-32 US-09-489-033A-8669 US-09-489-033A-8669 US-08-896-365-9 US-08-833-752-4 US-08-833-752-4 US-09-133-735-4 US-09-0813-752-6 US-09-0813-752-9	OF 0 - FF7 - 80 - 80
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                                                                    APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monse, Kelley L.
APPLICANT: Mand, Shelby P.
APPLICANT: Wang, Suke
ITLE REFERENCE: CN01069
CURRENT APPLICATION UNDBER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2. Application US/09812216
Fatent No. 661353
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Medrick, Joseph A.
APPLICANT: Morse, Kelley L.
APPLICANT: Morse, Kelley L.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
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Sequence 2, Application US/09414010
Patent No. 6204017
GENERAL INFORMATION:
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Andrew D.J. Goodearl and Sandra Glucksman
JENTION: Muscarinic Receptors and Uses Therefor
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                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                               5.4%; Score 21; DB 4; Length 390;
100.0%; Pred. No. 2e-11;
iive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
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Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street CITY: Boston STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                                                                                                                     93 TDYLLCTASVYNIVLISYDRY 113
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US-09-165-543-8
Sequence 8, Application US/09165543
Parent No. 609345,
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: (617)/#2-22.
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
FRNGTH: 19 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATMONIEY/AGENT INFORMATION:
    PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 742-4214
TTTTPAX: (617) 742-4214
TTTPAX: (617) 742-NO:
                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02109
                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-985-090-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                          US-09-812-216-2
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3.09-165-543-15
3.69quence 15, Application US/09165543
5.9quence 15, Application US/09165543
5.9quence 10. 6093545
6.9quence 10. 6093545
7.0quence 10. 6093545
7.0quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 600quence 10. 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11; DB 3; Pred. No. 0.0028;
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APPLICANT: Angle...
TITLE OF INVENTION: Muscal...
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 128 State Street
CITY: Boston Street
CITY: Boston State Street
CITY: Boston State Street
CITY: Boston State Street
CITY: Boston Street
CITY: Boston Street
COUNTRY: Boston State Street
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
COMPUTER: IBM PC COMPATINE
COMPUTER: IBM PC COMPATINE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LNLAISDFLVG 12
                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
: USA
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TOPOLOGY: linear
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Query Match 2.8%; Score 11; DB 2; Length 445; Best Local Similarity 100.0%; Pred. No. 0.045; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION WINBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECHONE: (6.77)227-7400
TELEPHONE: (6.77)277-7400
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 445 amino acidd TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 445 amino acids
amino acid
                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-985-090-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 LNLAISDFLVG 65
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MOLECULE TYPE: protein
US-09-165-543-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-165-543-2
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Sequence 2, Application US/08985090

Patent No. 5885893

APPLICANT: Andrew D.J. Goodearl

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
2.8%; Score 11; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%; Score 11; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 0.0028; Matches 11; Conservative 0; Mismatches 0; Indels
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Patent No. 6355452
GENERAL INFORMATION:
APPLICANT: PING TSUATION:
APPLICANT: PING TSUATION:
TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
FILE REFERENCE: GP-70681
CURRENT APPLICATION NUMBER: US/09/524,162
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Blizabeth A. Hanley
REGISTRATION NUMBER: 33,505
TREFERENCE/DCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRX: (617)227-7400
TELEFRX: (617)742-4214
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 LNLAISDFLVG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 LNLAISDFLVG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-524-162-2
                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                       US-09-165-543-15
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LENGTH: 351
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Gaps

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Sequence 2. Application US/09165543

Patent No. 6093545

GENERAL INFORMATION:

APPLICANT: ADDRESS:

APPLICANT: ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: IAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION UNDRER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
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Length 445;

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US-09-642-514-7; Sequence 7, Application US/09642514; Patent No. 6437100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 445
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                                                                                                                                                                                                                                                                              74 LNLAISDFLVG
         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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APPLICANT: Lovenberg, Timothy
APPLICANT: Evlander, Mark
APPLICANT: Byati, Jayashree
APPLICANT: Byati, Jayashree
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
                             Gaps
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                                                                                                                                                                                 Sequence 5, Application US/09165543
; Sequence 6. 6093545
; Patent No. 6093545
; GENERAL INFORMATION:
    APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
    TITLE OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%; Score 11; DB 3; Length 445; 100.0%; Pred. No. 0.045; ive 0; Mismatches 0; Indels
Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: PSYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REGISTRATION NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09167354A Patent No. 6136559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...

11, Conservative
                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-09-165-543-5
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                                                                                                                                                                                                                                                                                                                                     STREET: 28 State Stre
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                        55 LNLAISDFLVG 65
              Best Local Similarity
Matches 11; Conserva
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US-09-167-354-7
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US-09-165-543-5
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; Sequence 7, Application US/09642855
; Patent No. 4413743
; Patent No. 4413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Huvar, Arne
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: UNBER ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; TITLE OF INVENTION: UNBER: 09/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; RECREATE 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Elander, Mark
APPLICANT: Pyari, Jayashree
APPLICANT: Pyari, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT FILING DATE: 1998-10-06
PRIOR PILING DATE: 1998-10-06
                                                                                                                                          Gaps
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, OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE US-09-167-354-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 445;
                                                                               Length 445;
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2.8%; Score 11; DB 4; Length 445
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                               Query Match 2.8%; Score 11; DB 3; Length 445
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels
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NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
AADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-165-543-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.3
Best Local Similarity 100.
Matches 9; Conservative
                                                                                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 NIVLISYDR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COM
OPERATING SYSTEM:
                                    ADDRESSEE: LAH
STREET: 28 Sta
CITY: Boston
                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-833-226-2
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                                                                                                                                                                                                                                                                                                                     US-08-985-090-5

Sequence 5, Application US/08985090

Sequence 5, Application US/08985090

PERENT NO. 5885893

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl

TITLE OF INVENTION:

WUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                        ; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE US-09-642-514-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
                                                                                                                                2.8%; Score 11; DB 4; Length 445, 100.0%; Pred. No. 0.045; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 362;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 9; DB 2;
100.0%; Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MN.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)742-4214
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.0
Pest Secondarive 9; Conservative
                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                            55 LNLAISDFLVG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-985-090-5
                                                                                                                                                                                                                                       74 LNLAISDFLVG 84
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                                                                                                                                                Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02109
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LENGTH: 445
                                                                                                                                  Query Match
                                                    FEATURE:
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Gaps
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Patent No. 5891720
GENERAL INFORMATION:
APPLICANT: Moore, Karen
APPLICANT: Moolf, Bizabeth
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 9; DB 3;
100.0%; Pred. No. 2.7;
tive 0; Mismatches
                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Blizabeth A. Hanley,
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: 33,505
TELECOMINICATION INFORMATION:
TELEFONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CUNNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,226
FILING DATE: 17-APR-1997
CLASSIFICATION: 514
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Length 384;
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Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches
REFERENCE/DOCKET NUMBER: 7853-080
TELECOMMUNICATION INFORMATION:
TELEFANE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS:
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
WOLECULE TYPE: protein
US-08-833-226-2
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Search completed: October 1, 2004, 10:30:22 Job time : 33 secs

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0; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 1, 2004, 10:29:06 ; Search time 134 Seconds (without alignments) 938.981 Million cell updates/sec

1 MSESNSTGILPPAAQVPLAF......WKILCVTKWPALSQNQSVSS 391 US-10-626-445-8 391 Perfect score: Sequence:

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1351062 seqs, 321799191 residues Searched:

0 Word size :

1351062 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	* [] *] * [Sequence 6. Appli	Sequence 2. Appli	Semience 2 Annli	Semience & annih	Semience o Applia	٠,۲	, ,	Sequence 11, Appli	Semience 2, Applit	Segmence 22 and	Segmente 14 Appl	Segmence 11, Appr	Somioned 14 Applie	Sequence 14, Appr	sednence 14, Appl	Sequence 2, Appli	
		ID		US-09-782-974C-6	US-09-910-411-2	US-09-852-165-2	US-09-891-138A-6	US-10-349-253A-2	US-09-875-076-14	US-09-876-252-14	US-10-052-193-2	US-10-225-567A-629	US-10-290-078-27	US-10-272-983-14	US-10-354-769-2	11S-10-193-807-14	TE-10-417-0208 14	#T-W070-17#-07-00	US-10-696-673-2	
		DB	1 1 1	10	ص	10	10	77	12	12	13	14	14	14	14	14	ינ	7	16	
		Match Length DB	1 1 1 1 1 1	73	390	390	390	390	390	390	390	390	390	390	390	390	000) (390	
æ	Query	Match		5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	2		5.4	
		Score	1111111	21	21	21	21	21	21	21	21	21	21	21	21	21	21	1 6	77	
	Result	No.	· · · · · · · · · · · · · · · · · · ·	-	5	m	4	D.	9	7	æ	6	10	11	12	13	14	1 .	CT	

Sequence 14, Appl	~	H	m	8	. 1	00	15	Seguence 8. Appli	15	е 8	-	7	4		Sequence 5. Appli	ς.	S	Sequence 2, Appli	Ŋ	a			54	H	7	'n	7	20	Sequence 13, Appl
US-10-	16 US-10-737-619-2	-59	US-10-398-0	1		1-349-755-	US-09-349-7	99-166	9 US-09-166-334-15	14 US-10-282-958-8	- 1	10 US-09-791-279-147	12 US-09-891-053-1		39-3	US-09-349-75	US-09-34	-166-3	9 US-09-166-334-5	12 US-09-891-053-25			14 US-10-225-567A-549	16 US-10-453-106-1	16 US-10-453-106-2	16 US-10-453-106-3	16 US-10-727-021-7	-09-891-	14 US-10-067-649-13
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16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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CURRENT FILING DATE: 2002-09-04

PRICA APPLICATION NUMBER: 60/165,838

PRICA PAPLICATION NUMBER: 60/165,838

PRICA PAPLICATION NUMBER: 60/165,838

PRICA FILING DATE: 2000-01-16

PRICA FILING DATE: 2000-01-16

PRICA FILING DATE: 2000-01-16

PRICA PAPLICATION NUMBER: 60/166,071

PRICA PLILING DATE: 2000-04-20

PRICA PLILING DATE: 1999-11-19

PRICA PLILING DATE: 1999-11-19

PRICA PLILING DATE: 1999-11-19

PRICA PLILING DATE: 1999-11-19

PRICA PLILING DATE: 1999-11-28

PRICA PLILING DATE: 1999-12-28

PRICA PLICATION NUMBER: 60/184,129

PRICA PLILING DATE: 2000-02-26

PRICA PLICATION NUMBER: 60/185,554

PRICA PLICATION NUMBER: 60/186,530

PRICA PLICATION NUMBER: 60/186,530

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PRICA PLICATION NUMBER: 60/186,530

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PRICA PRICATION NUMBER: 60/186,530

PRICA PRICATION NUMBER: 60/186,530

PRICA PRICATION NU
                                                                                                     Sequence 6, Application US/09782974C
Publication No. US20030082534A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
FILE REFERENCE: 411USPHRM311
RESULT 1
US-09-782-974C-6
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RESULT 5
US-10-349-253A-2
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Publication No. US20030032784A1
GENERAL INFORMATION:
APPLICANT: Lind, Peter
APPLICANT: Wogeli, Gabriel
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20030032784A1e1 G Protein-Coupled Receptors
FILE REFERENCE: 00231regUS
CURRENT APPLICATION NUMBER: US/09/852,165
CURRENT PILING DATE: 2001-05-08
PRIOR FILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-05-08
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; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
    APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgrald, Laura
    APPLICANT: Li, Xiatong
    APPLICANT: Li, Xiatong
    APPLICANT: Xia, Yuan
    TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
    FILE REFERENCE: GP70655-21
; CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2001-07-20
; PRIOR PELICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-03
; PRIOR PELICATION NUMBER: 09/497,790
; PRIOR PELING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; NUMBER OF SEQ ID NOS: 2
; NUMBER OF SEQ ID NOS: 2
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                                                                           Query Match 5.4%; Score 21; DB 10; Length 73; Best Local Similarity 100.0%; Pred. No. 3e-12; Matches 21; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENOTH: 390
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Best Local Similarity 100.0
Matches 21; Conservative
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ORGANISM: Homo sapiens
                    ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
                                           US-09-782-974C-6
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US-09-910-411-2
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TYPE: PRT
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100.0%; Pred. No. 1.3e-11;
tive 0; Mismatches 0; Indels
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APPLICANT: Bergsma, Derk
APPLICANT: Elegerald, Laura
APPLICANT: Fitzgerald, Laura
APPLICANT: Graybill, Todd
APPLICANT: Morrow, Dwight
APPLICANT: Morrow, Dwight
APPLICANT: Morrow, Dwight
APPLICANT: Morrow, Dwight
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C2
CURRENT APPLICATION NUMBER: US/10/349,253A
CURRENT APPLICATION NUMBER: 09/910,411
PRIOR APPLICATION NUMBER: 09/910,411
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR PLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
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PRIO
         Length 390;
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Sequence 6, Application US/09891138A

Sequence 6, Application US/09891138A

Sequence 7, Application Wo. US20030083245A1

APPLICANT: Lin, Daniel Chi-Hong

APPLICANT: Chen, Jin-Long

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: Cutler, Gene

APPLICANT: WINSTER INC.

CURRENT APPLICATION NUMBER: US/09/891,138A

CURRENT APPLICATION NUMBER: US 60/213,461

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 390
5.4%; Score 21; DB 10; I
100.0%; Pred. No. 1.3e-11;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 21; Conservative
             Query Match 5.4
Best Local Similarity 100.
Matches 21; Conservative
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, 1-Lin
APLICANT: Lin, 1-Lin
FITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOSSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR PAPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/121,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR PILING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-13
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Publication No. US20030017528A1
GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Homo sapien
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APPLICANT: Chem, Ruoping
APPLICANT: Liaw, Chem W.
TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled RecePILE REFERENCE: AREN-0054
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Pred. No. 1.3e-11;
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CURRENT FILING DATE: 2001-06-07
PRIOR FULING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR PELLOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR PELLOR DATE: 1999-03-12
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PRIOR APPLICATION NUMBER: 60/136,436
PRIOR PELLOR DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
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PRIOR PELLOR DATE: 1999-05-28
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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Lin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
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US-09-876-252-14
IS-09-876-252-14

Sequence 14, Application US/09876252
Publication No. US20030018182A1
GENERAL INFORMATION:
; ORGANISM: Homo sapiens
US-09-875-076-14
                                                                                            Query Match
Best Local Similarity
Matches 21; Conserv
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Sequence 27, Application US/10290078

Publication No. US20030124596A1

GENERAL INFORMATION:

APPLICANT: Carroll, Joseph A.

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 10630, 13875,

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TITLE OF INVENTION: Hematological Disorders Using 232, COS9, 13875,

TITLE OF INVENTION: Hematological Disorders
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US-10-272-983-14
Sequence 14, Application US/10272983
Sequence 14, Application US/10272983
Publication No. US2030148450A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARBNO050
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-0-16
PRIOR FILING DATE: 1999-0-2-16
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100.0%; Pred. No. 1.3e-11;
tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 629
LENGTH: 390
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Best Local Similarity 100.(
Matches 21; Conservative
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Best Local Similarity 100.0
Matches 21; Conservative
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CRGANISM: Homo sapiens
US-10-225-567A-629
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) ORGANISM: Homo Sapien
US-10-290-078-27
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%; Score 21; DB 12; Length 390;
100.0%; Pred. No. 1.3e-11;
tive 0; Mismatches 0; Indels
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JERUSALI HINTORNALION:
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
TITLE REPERENCE: PC109618R: US/10/052,193
CURRENT APPLICATION NUMBER: US/10/052,193
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALCENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 390
               PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR PILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR PRILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR PILING DATE: 1999-10-01
PRIOR SPELICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-10-01
PRIOR SPELICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-10-01
PRIOR SPELICATION NUMBER: 60/156,633
PRIOR PRILING DATE: 1999-100-01
PRIOR SPELICATION NUMBER: 60/156,633
PRIOR PILING DATE: 1999-100-01
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; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
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Publication No. US20020132755A1
GENERAL INFORMATION:
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Matches 21; Conservative
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; ORGANISM: Homo sapiens
US-10-052-193-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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93 TDYLLCTASVYNIVLISYDRY 113
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Best Local Similarity 100.0%; P. Matches 21; Conservative 0;
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PRIOR APPLICATION NUMBER: 60/136,436

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR PLING DATE: 1999-05-28

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PROMINING PRIOR APPLICATION NUMBER: 60/136,567

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

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100.0%; Pred. No. 1.3e-11;
Live 0; Mismatches 0; Indels
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Sequence 2, Application US/10354769
Sequence 2, Application US/10354769
Sequence 2, Application US/10354769
Sequence 2, Application US/10354769
SERRAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: P(Reilly, Mark A.
APPLICANT: Perer. Beate
ITILE OF INVENTION: NOVEL POLYPEPTIDE
FILE REFRENCE: P(373B
CURRENT APPLICATION NUMBER: US/0/354,769
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/211,243
PRIOR APPLICATION NUMBER: US 60/211,243
PRIOR APPLICATION NUMBER: US 60/211,243
PRIOR APPLICATION NUMBER: GB 9925641.4
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: GB 9925641.4
PRIOR FILING DATE: 2000-06-16
SPRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 10
SOFTWARRE: PATENTIN VENSION 3.1
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US-10-393-807-14
; Sequence 14, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
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Matches 21; Conservative
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APPLICANT: Dang, Huong T
APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 390
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Sequence 14, Application US/10417820A

Publication No. US20030229216A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

FILE REFERENCE: 7.US28.CON

CURRENT APPLICATION NUMBER: US/10/417,820A

CURRENT APPLICATION NUMBER: 09/416,760

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13

PRIOR PLING DATE: 1999-02-26

PRIOR PLING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-10-23

PRIOR PLICATION NUMBER: 60/120,416

PRIOR PLICATION NUMBER: 60/120,213

PRIOR PLICATION NUMBER: 60/120,213

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-03-8

PRIOR FILING DATE: 1999-03-8

PRIOR FILING DATE: 1998-11-20

PRIOR FILING DATE: 1998-11-20
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TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOOSO
CURRENT APPLICATION NUMBER: US/10/393,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21; DB 14; Length 390;
Pred. No. 1.3e-11;
0; Mismatches 0; Indels
                                                                                                       CURREMA APPLICATION NUMBER: US/09/10/2007/
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-10-2
PRIOR FILING DATE: 1999-02-16
PRIOR PILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-03-12
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RESULT 15

US-10-696-673-2

Sequence 2, Application US/10696673

Sequence 2, Application US/10696673

Sequence 2, Application Wo. US20040105846A1

GENERAL INFORMATION:
APPLICANT: Dind, Peter
APPLICANT: Dind, Peter
APPLICANT: Woedli, Gabriel
APPLICANT: Wood, Linda 8

TILE REFERENCE: PHEMO025-101/00231REGUS.1 DV1
CURRENT APPLICATION NUMBER: US/010/696,673

CURRENT PILING DATE: 2000-10-28

PRIOR APPLICATION NUMBER: US 60/203,108

PRIOR APPLICATION NUMBER: US 60/203,108

PRIOR APPLICATION NUMBER: US 09/852,165

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 3

SEQ ID NO 2

LENGTH: 390
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PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
LENGTH: 390
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, ORGANISM: Homo sapiens
US-10-696-673-2
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US-10-417-820A-14
                                                                                                                                                                                                                                              TYPE: PRT
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Search completed: October 1, 2004, 10:41:05 Job time : 135 secs

93 TDYLLCTASVYNIVLISYDRY 113

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October 1, 2004, 10:23:00; Search time 41 Seconds (without alignments) 917.339 Million cell updates/sec
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                                                                                                                                                                          US-10-626-445-8
391
1 MSESNSTGILPPPAQVPLAF......WKILCVTKWPALSQNQSVSS 391
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                   - protein search, using sw model
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	Description	١,	amilie H4	Τ,	-		procein secretion	Wassignacety1-coa I	euramır	T :	i,	-4	hypothetical prote	_	hypothetical prote	melatonin receptor	conserved hypothet	hypothetical prote		,		Thetian nee	٦,	himothotical acces		transcri	peptide	lein	Liyptophan synthas		e procein-coupled peroxidase (EC 1.1
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Cispecies: Brucella melitensis (strain 16M)
Cispecies: Brucella melitensis
Cipate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 02-Aug-2002
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A,Gene: BMEII0111 A,Map position: II C,Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase cpdA; 3',5'-cyclic-nucleotide pt

Length 281;

DB 2;

2.0%; Score 8;

Query Match

A.Accession: AE3523 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-281 <KUR> A.Cross-references: GB:AE008918; PIDN:AAL53352.1; PID:g17984241; GSPDB:GN00191

Nosx protein requipolygalacturanase-Mel-la melatonin rehemokine (C-C) reopsin, rod ultravichemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) rechemokine (C-C) remokine (C-C) rechemokine (C-C) rechemokine (C-C) re	RESULT 1 JUC7566 Holstamine H4 receptor, HH4R - human C.Decies: Homo sapiens (man) C.Decies: Homo sapiens (man) C.Decies: Homo sapiens (man) C.Decies: Homo sapiens (man) C.Decies: J0-Jun-2001 Hsquamura, T.: Itadani, H.: Hidaka, Y.: Ohta, M.: Tanaka, K. Biochem. Biophys. Res. Comun. 279, 615-620, 2000 A:Title Molecular cloning and characterization of a new human histamine receptor, HH4R. A:Title Molecular Cloning and characterization of a new human histamine receptor, HH4R. A:Totents: Leukocyte A:Contents: Leukocyte A:Goneris: Leukocyte A:Goneris: DBJ:AB045370 C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: A:Goneris: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Goment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A:Genetics: C:Gonery Match C:Goner	
H95342 S23764 138848 A43113 A43113 A45129 G02432 G02443 A45177 A45160 A45177 A45160 JC2443 JC2443 JC2443 JC4692 JC4692 JC4692 JC4646 A3933 A39234		Y 113
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3344 344 3460 3460 3460 3460 3460 3460 3	receptor, HH4R - humar no sapiens (man) 10756 / Itadani, H.; Hidaka yys. Res. Commun. 279, uys. Res. Commun. 279, uys. Res. Commun. 279, uys. Res. Commun. 279, us. Commun. 279, us. Commun. 279, us. Complete Res. see mRNA 390 CNRK. see mRNA 390 CNRK. seeptor, belonging protein-coupled recep protein-coupled recep protein-coupled recep imilarity 100.0%; conservative 0, TDYLLCTASVYNIVLISYDRY	IDKLLCIASVYNIVLISYDRY
	4 receptor, Jun-2001 #se Jun-2001 #se JC756 JC756 JC756 JC756 JC756 JC756 JC756 JC756 JC756 JC76	LCIAS
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	H4 re H10mc	
8	RESULT 1 JC7566 histamine H4 receptor, HH4R - human C;Date: 30-Jun-2001 #sequence_revis: C;Accession: JC7566 R;NARamura, T.; Itadani, H.; Hidaka, Biochem: Biochys. Res. Commun. 279, A;Title: Molecular cloning and chars. A;Reference number: JC7566; MUID: 20, A;Contents: Leukccyte A;Accession: JC7566 A;Molecule type: mRNA A;Residues: 1-390 ANRA: A;Residues: 1-390 ANRA: A;Gonerics: DBB:AB045370 C;Comment: This receptor, belonging C;Genetics: Dh4r C;Keywords: G protein-coupled recept Query Match Best Local Similarity 100.0%; P Matches 21; Conservative 0; Oy S; TDYLLCTASVYNIVLISYDRY D)	3

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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: H75578
R;Mnite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P.R;Mnite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mah, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-426 <WHI>
A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12384.1; PID:g646067
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (EC 2 (Spate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2003 (Spate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2003 (Spate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2003 (Spate: 1, 7 ransshiro, S.; Yodoi, J.; Lloyd, K.O.; Shiku, H.; Furukawa, K. J. Ringata, Y.; Yamashiro, S.; Yodoi, J.; Lloyd, K.O.; Shiku, H.; Furukawa, K. J. Biol. Chem. 267, 12082-12089, 1992 A;Title: Expression cloning of beta 1,4 N-acetylgalactosaminyltransferase cDNAs that det A;Reference number: A44128; MUID:92291088; PMID:1601877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Status: preliminary
A.Status: mRNA
A.Molecule type: mRNA
A.Residues: 1-561 «NAG»
A.Experimental source: NK-like cell line YT
A.Store: sequence extracted from NCBI backbone (NCBIN:106611, NCBIP:106612)
C.Superfamily: (N-acerylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyl)txi
C.Superfamily: (N-acerylneuraminyl)-galactosylglucosylceramide protein
C.Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
                                                                                                                        A;Molecule type: DNA
A;Residues: 1-400 <DEG>
A;Cross-references: EMBL:X81085; NID:g3293032; PIDN:CAA56981.1; PID:g531742
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                      Indels
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Ride Groot, A.; Krijger, J.J.; Filloux, A.; Tommassen, i. Mol. Gen. Genet. 250, 491-504, 1996
A;Title: Characterization of type II protein secretion A;Reference number: S64724; MUID:96186881; PMID:8602167
A;Accession: S64729
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Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches
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8.8;
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0; Mismatches
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Matches 8; Conservative 0; Mismat
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C; Superfamily: coenzyme F390 synthetase II
                                                                                                                                                                                                                                                                      C; Superfamily: secretion protein xcpS
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C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 20-Jun-2000
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 20-Jun-2000
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 20-Jun-2000
C;Accession: A55450
R;Saito, K.; Tatsuguchi, K.; Takagi, Y.; Murakoshi, I.
J. Biol. Chem. 269, 28187-28192, 1994
A;Title: Isolation and characterization of cDNA that encodes a putative mitochondrion-1c
A;Reference number: A55450; MUID:95050598; PMID:7961755
A;Accession: A55450; MUID:95050598; PMID:7961755
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A;Molecules: prep; DNA
A;Residues: 1-328 <WILb>A;Cross-references: EMBL:Z49967; PIDN:CAA90256.1; GSPDB:GN00020; CESP:F54C9.11
A;Experimental source: clone F54C9
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C;Species: Pseudomonas putida
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2000
(C;Accession: S64729; S47506
                                                                                                                                                                                                                                                                              hypothetical protein F54C9.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22636
R;Sims, M.
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                                                          Indels
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100.0%; Pred. No. 8.2;
iive 0; Mismatches
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100.0%; Pred. No. 7.4;
attive 0; Mismatches
                                  red. No. 6.4;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1995 A;Reference number: Z19591 A;Accession: T22636
                                     Pred. No.
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                                        100.08;
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                   191 ASGHLHRA 198
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nes 8; Conserv
                                     Best Local Similarity
Matches 8; Conserv
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A;Introns: 24/2; 92/3
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S64729
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Pred. No. 12;

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C.Superfamily: Neisseria meningitidis hypothetical protein NMA1503
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100.0%; Pred. No. 26;
cive 0; Mismatches
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1.8%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity
7; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: NMA1503
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A.Note: Nostoc sp. PCC 7120

A.Note: Nostoc sp. PCC 7120

A.Note: Nostoc sp. strain PCC 7120

A.Note: Nostoc sp. strain PCC 7120

C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C.Accession: AE2381

R.Karaeko, T. Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

DNA Res. 8, 205-213, 2001

A.Yitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A.Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein asr1234 [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. ptc 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1960
C;Accession: AG1960
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A;Molecule type: DNA
A;Residues: 1-55 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB76304.1; PID:g17133742; GSPDB:GN00179
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                histone H1 - sea urchin (Strongylocentrotus intermedius) (fragment)
C;Species: Strongylocentrotus intermedius
C;Date: 17-Jul-1392 #sequence_revision 17-Jul-1992 #text_change 12-Apr-1995
C;Accession: B38839
                                                                       Gaps
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J. Biochem. 108, 347-355, 1990
A'Title: Sea urchin protease specific to the SPKK motif in histone.
A'Reference number: PS0145; MUID:91115778; PMID:2126010
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100.0%; Pred. No. 15;
100.0%; Preq. ....
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100.0%; Pred. No. 9.4
tive 0; Mismatches
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tive 0; Mismatches
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A;Residues: 1-32 <SUZ>
C;Superfamily: histone H1
C;Keywords: chromosomal protein; nucleosome
                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 7; Conservative
                                                                                                              219 STISSSAS 226
                                                                                                                                                                                  STTSSSAS 426
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          Best Local Similarity
Matches 8: Conserv
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Best Local Similarity
Matches 7; Conserv
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A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anai A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AG1960
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-98 «KUR>
A; Residues: 1-98 «KUR>
A; Experimental source: Strain PCC 7120
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein NMA1503 [imported] - Neisseria meningitidis (strain 22491 serogroup Gibbecies: Neisseria meningitidis
Gibbecies: Neisseria meningitidis
Gibate: 05-May-2000 #text_change 02-Feb-2001
Gibate: 05-May-2000 #text_change 02-Feb-2001
Riparkhili. J. Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell Nature 404, 502-506, 2000
A; File: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-103 <PAR>
A/Residues: 1-103 <PAR>
A/Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84735.1; PID:g738015(
A/Experimental source: serogroup A, strain Z2491
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
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A;Residues: 1-108 <TET>
A;Cross-references: GB:AE002478; GB:AE002098; NID:g7226533; PIDN:AAF41669.1; PID:g7226534
A;Experimental source: serogroup B, strain MC58
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C;bacies: Neisseria meningitidis
C;bate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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Search completed: October 1, 2004, 10:29:45
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T16798
hypothetical protein T04A6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16798
R;Vaudin, M.; Anderson, K.
submitted to the EMBL Data Library, April 1994
A;Description: The sequence of C. elegans cosmid T04A6.
A;Reference number: Z18579
A;Accession: T16798
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-111 «VAU»
A;Residues: 1-111 «VAU»
A;Residues: EMBL:U00042; NID:9470332; PID:9470333; PIDN:AAA50672.1; CESP:T04A6.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Genetics:
A;Hurrons: 11/3; B2/1
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melatonin receptor - striped hairy-footed hamster (fragment)
C;Species: Phodopus sungorus (striped hairy-footed hamster)
C;Species: Phodopus sungorus (striped hairy-footed hamster)
C;Species: Phodopus sungorus (striped hairy-footed hamster)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1397 #text_change 20-Apr-2000
C;Accession: 184498
R;Reppert, S.M.; Weaver, D.R.; Ebisawa, T.
Neuron 13, 1177-1185, 1994
A;Accession: 184898
A;Title: Cloning and characterization of a mammalian melatonin receptor that mediates re
A;Accession: 184898
A;Accession: 184898
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A;Accession: 184898
A;Accession: 184808
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C;Superfamily: vertebrate rhodopsin
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Matches 7; Conservative 0; Mismatches
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    Query Match 1.8%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A.Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83307
A;Status: preliminary
A;Aolecule type: DNA
A;Residues: 1-159 cSTO-
A;Cross-references: GB:AE004699; GB:AE004091; NID:g9948782; PIDN:AAG06101.1; GSPDB:GN001:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2713
Query Match
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Hapsial 20
Db 14 ARSLAIL 20
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	DAN STANDARI O902200; C001 (Rel. 40, C001 (Rel. 43, Inc. 1004 (Rel. 44, Inc. 1004 (Rel	ophil; 4636; Pu Behan J. Umland L., Qiao Jr.; charact Exp. T
2333 2444 2444 277 2444 2544 2544 2544 2544	HHAR HUMAN HHAR HUMAN HHAR HUMAN HHAR HUMAN G9H3NB, Q9GZQ0; 16-OCT-2001 (Rel. 40, L. 15-NAR-2004 (Rel. 43, L. 15-NAR-2004 (Rel. 43, L. 15-NAR-2004 (Rel. 43, L. 15-NAR-2004 (Rel. 43, L. 15-NAR-2004 (Rel. 43, L. 15-NAR-2004 (Rel. 43, L. 16-OCT-2001 (Rel. 43, L. 16-OCT-2001 (Rel. 43, L. 15-NAR-2004 (Rel. 43, L. 16-OCT-2004 (Rel. 43, L. 16-OCT-2004 (Rel. 43, L. 16-OCT-2004 (Rel. 43, L. 17-NAR-2004 (Ruman). MOBIL TAXID=5066; [1] MOBIL TAXID=5066; [1] MOBIL TAXID=5066; [1] MOBIL TAXID=206814; MOBIL TAXID=206817; MOBIL TAXID=20687; MOBIL TAXID=20687; MOBIL TAXID=20687; MOBIL TAXID=2068725; PubMed T., MORING T. MOBIL TAXID=2068725; PubMed T., NAND (RELINE 2068725; PubMed T., NAND (RELINE 2068725; PubMed T., NAND (RELINE 2068725; PubMed T., NAND (RELINE EROM N.A., AND (REUMB C.), NAND (REUMB C.), NAND (REUMB C.), NAND (REUMB C.), NAND (REUMB C.), NAND (REUMB C.), NAND (RECEPTOR (HA) EXPLESSED (HA) EXPLESSED (HA) EXPLESSED (HA) EXPLESSED (HA) EXPLESSED (HA) EXPLESSED (HA) EXPLESSED (HA) EXPLESSED EXPLAND (RESPONDED FROM N.A., AND (RELINE RESPONDED FROM N.A., AND (RELINE RESPONDED FROM N.A., AND (REUMB FROM N.A., AND (REUMB FROM	TISSUE-Eccinomy, Management of the Medium of
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[6] SEQUENCE FROM N.A. MEDLINE=21106320; PubMed=11179436;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                      Pull H.L. III, Ikeda S.R., Aronstam R.S.; signal transduction "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (JUL_2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUL_2002) to the EMBL/GenBank/DDBJ databases. - FUNCTION: The H4 subclass of histamine receptors could mediate the histamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the
                                                                                                                                              0'Reilly M.A.; "Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis."; "Interest of the cosinophil chemotaxis.";
Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J., Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L., Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S., Bergsma D.J., Fitzgerald L.R.; "Cloning, expression, and pharmacological characterization of a novel human histanine receptor."; Mol. Pharmacol. 59:434-441(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                     in eosinophil chemotaxis.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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EMBL; AB045370; BAB20091.1; -.
EMBL; AF307973; AAG32052.1; -.
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EMBL; AJ298292; CAC83493.1;
EMBL; AY136745; AAN01271.1;
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EMBL; AF325356; AAL01684.1;
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Genew; HGNC:17383; HRH4.
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MEDLINE=20218440; PubMed=10757514;
Tardivel-bacombe J., Rouleau A., Heron A., Morisset S., Fillot C.,
Tardivel-bacombe J., Rouleau A., Heron A., Morisset S., Fillot C.,
Tardivel-bacombe J., Rouleau J.-M.;
Icohing and cerebral expression of the guinea pig histamine H3
receptor: evidence for two isoforms.";
NeuroReport 11,755-759(2000).
                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
S-palmitoyl cysteine (Potential).
A -> V (IN REF. 1).
H -> R (IN REF. 1).
Q -> R (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
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Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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                  PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                       EXTRACELLULAR (POTENTIAL) .
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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(POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                CYTOPLASMIC (POTENTIAL).
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Name=Long; Synonyms=H3L;
Isofd=Q9u135-1; Sequence=Displayed;
Name=Short; Synonyms=H3S;
Name=Short; Synonyms=H3S;
Isold=Q9J135-2; Sequence=VSP_001880;
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Last annotation update)
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N-LINKED (GLCNA
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100.0%; Pred. No.
rative 0; Mismatc
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Cavia porcellus (Guinea pig).
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PR00237; GPCRRHODOPSN.
PR01726; HISTAMINEH4R.
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H3

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Cloning and functional expression of the human histamine
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE SPECIFICITY: Expressed widely and abundantly throughout the brain. Highly expressed in discrete neuronal populations such as pyramidal cells in cerebral cortex or cerebellar purkinje cells. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Huvar A., Jackson M.R., Erlander M.G.;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Histamine H3 receptor (HH3R) (G protein-coupled receptor 97)
HRH3 OR GPCR97.
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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BAE206A3887189A0 CRC64;
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MEDLINE~99278519; PubMed=10347254;
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InterPro; IPR003980; H3_receptor.
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PRINTS; PR01471; HISTAMINEH3R.
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nes 11; Conservative
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Mediciar S. P., Matthews. I. H., Shurst J., Burton J., Gilbert J.G.R., An Deloukas P., Matthews. I. H., Shurst J., Burbage A.K., Bagguley C.L., Bailey W. R., Bates K.N., Barde L.M., Beare D.M., Beasley O.P., Bird C.P., Blackey S.E., Bridgeman A.M., Brown A.J., Back D.M., Clark G.Y., Barter A.P., Carder C., Carter N.P., Carder C., Carter N.P., Cleng M., Clark G.Y., Clee C.M., Clegg S., Cobley V.E., Collare R.E., Cornor R.E., Corby N.R., Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Blington A.G., Frankland J.A., Fraser A., French L., Garner P., Blington A.G., Frankland J.A., Fraser A., French L., Garner P., Carterin B.D., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammend S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Hammend S., Harley J.L., Meath P.D., Ho S., Holden J.L., Howden P.J., Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., A. Marsh V.L., Marth S.L., McConnachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., McCannachle L.J., Thomas D.W., Taylor R., Sehra H.K., Shownken R., Sims S., Swann R.M., Scott C.E., Sehra H.K., Shownken R., Sims S., Swann R.M., Scott C.E., Sehra H.K., Shownken R., Sims S., Swann R.M., Scott C.E., Sathra H.K., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R., Shownken R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P., Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P., "Genomic organization and characterization of splice variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and comparative analysis of human chromosome 20.";
                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZALLON.
MEDLINE=20568725; PubMed=11118334;
Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
"Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=11953383; PubMed=11956964; Wiedemann P., Boenisch H., Oerters F., Bruess M.; "Structure of the human histamine H3 receptor gene (HRH3) and identification of naturally occurring variations."; [5] Neural Transm. 109:443-453(2002).
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Ullmer C., Zirwes E., Lubbert H.;
"Cloning and functional expression of the human histamine H3S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).
                                                                                                                                                                                                                                                                                                                                                                                receptor, HH4R.";
Biochem. Biophys. Res. Commun. 279:615-620(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thalamus;
MEDLINE=21181559; PubMed=11284713;
receptor.";
Mol. Pharmacol. 55:1101-1107(1999)
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MEDLINE=21638749; PubMed=11780052;
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Biochem. J. 355:279-288(2001)
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DR EMBL; AR140538; BAB20090.1; -
DR EMBL; A8045369; BAB20090.1; -
DR EMBL; A8045369; BAB20090.1; -
DR EMBL; A8045369; BAB20090.1; -
DR EMBL; A1296622; CAC51025.1; -
DR EMBL; A1278250; CAC51025.1; -
DR EMBL; A1278250; CAC51025.1; -
DR EMBL; A1278250; CAC51025.1; -
DR EMBL; A1278250; CAC51021.1; -
DR Genew; HGNC:5184; HRH3.

DR MIM; 146500; -
DR GO; CO0005897; C:integral to plasma membrane; TAS.

DR GO; GO:00004869; E:instandine receptor activity; TAS.

DR GO; GO:0000187; P:G-protein signaling; coupled to cyclic nucl. .; TAS.

DR GO; GO:0000187; P:G-protein signaling; coupled to cyclic nucl. .; TAS.

DR GO; GO:0000187; P:G-protein signaling; coupled to cyclic nucl. .; TAS.

DR GO; GO:0000187; P:G-protein signaling; coupled to cyclic nucl. .; TAS.

DR FROSTE; PRO0023; GFCRRHODOPS.

DR PROSTE; PSO023; GPCRRHODOPS.

DR PROSTE; PSO023; GPCRRHODOPS.

DR PROSTE; PSO023; GPCRRHODOPS.

DR PROSTE; PSO023; GPCRRHODOPS.

DR PROSTE; PSO023; GPROTEIN RECEP FI. 1; 1.

DR PROSTE; PSO023; GPROTEIN RECEP FI. 2; 1.

KW Alternative splicing; Disease mutation.

THE TOWNIN IN THE TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWNING TOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                           -I-TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the greatest expression in the thalamus and caudate nucleus. The various isoforms are mainly coexpressed in brain, but their relative expression level varies in a region-specific manner. Isoforms 3 and 7 are highly expressed in the thalamus, caudate nucleus and carebellum while isoforms 5 and 6 show a poor expression. Isoforms 5 and 6 show a high expression in the amygdala, substantia nigra, cerebral cortex and hypothalamus. Isoform 7 is not found in hypothalamus or substantian nigra.
-!- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome [MIM:146500]. This syndrome is characterized by orthostatic hypotension, bladder and bowel incontinence, anhidrosis, iris arcophy, amyotrophy, ataxia, rigidity and tremor.
-!- MISCELLANEOUS: Does not bind to cimetidine and tripolidine. Shows modest affinity for thioperamide, imetit, N-alpha-methylhistamine and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to indoproxyfan while isoforms 1 and 3 bind it with high affinity.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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Event=Alternative splicing; Named isoforms=7; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9Y5N1-6; Sequence=VSP 001883;
                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9Y5N1-7; Sequence=VSP_001884;
                                                                                                                                                                                                                                                          IsoId=Q9Y5N1-4; Sequence=VSP_001881;
                                                                                                                                                                                                                                                                                  Name=5;
IsoId=Q9Y5NI-5; Sequence=VSP_001882;
                                                                                                                                            IsoId=Q9Y5N1-2; Sequence=VSP_001886;
                                                                                                                                                                 Name=3; Synonyms=H3S;
IsoId=Q9YSN1-3; Sequence=VSP_001885;
                                                                                     IsoId=Q9Y5N1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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CYTOPLASMIC (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coge F., Rique H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,
Galizzi J.-P.;
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                           POLY-GLY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

Missing (in isoform 4).

Frid-VSP_001881.
                                                                                                                                                               Missing (in isoform 7).
/FITGHOSP 001884.
Missing (in isoform 3).
/FITGHOSP 001885.
K -> KRWKKYTCL (in isoform 2).
/FITGHOSP 001886.
A -> V (IN SHY-DRAGER SYNDROME).
/FITGHOSP 01235.
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                            2.8%; Score 11; DB 1; Length 445; 100.0%; Pred. No. 0.0042; tive 0; Mismatches 0; Indels
           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                      FTIG=VAR 012235.
-> D (IN REF. 1 AND 5).
2ACF7440FBE95B6C CRC64;
                                                EXTRACELLULAR (POTENTIAL)
                            CYTOPLASMIC (POTENTIAL).
                                                                                                                             (In isoform 5).
                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histamine H3 receptor (HH3R).
                                        POTENTIAL.
                                                                                                                                     Missing
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                                                                                                                                                                                                                                                           48671 MW;
                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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445 AA;
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SEQUENCE FROM N.A.
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3360
3381
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2250
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2250
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P58406;
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CARBOHYD
VARSPLIC
TRANSMEM
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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N-LINKED (GLCNAC. . .) (FOTENTIAL)
BBD406E29E1F3C5F CRC64;
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Pred. No. 0.0042;
0; Mismatches 0; Indels
                                                                                                                                              EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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Itadani H., Takimura T., Nakamura T., Ohta M.;
"Cloning of a novel G protein-coupled receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIR RAT STANDARD; PRT; 445 AA. OSQYNB; OSQYNB; OSQYNB; OSQYN7; OSQYNB; 28-FEB-2003 (Rel. 41, Created) CF-EB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Histamine H3 receptor (HH3R).
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ive 0; Mismatches
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                                                                                                            InterPro, IPR00376; GPCR Rhodpsn.
InterPro, IPR003980; H3_receptor.
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                                  EMBL; AY044153; AAK72406.1; -.
MGD; MGI:2139279; Hrh3.
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TISSUE=Hypothalamus;
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                                                                                       Isoid-090XN8-4; Sequence-VSP 001888, VSP 001889; TISSUE SPECIFICITY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform 1 is largely predominant in all tissues. MISCELIANEOUS: Proxyfan acts as a potent neutral antagonist while thioperamide, ciproxifan and FUB465 act as potent inverse
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                     MEDLINE=99278519; PubMed=10347254;
Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J., Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00277, G PROTEIN RECEP F1 1, 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2, 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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                                                                                                                                                                                   SÜBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                                                                                                            Name=3;
IsoId=Q9QYN8-3; Sequence=VSP_001888;
                                                                                                                                                                                                                                                     IsoId=Q0QYN8-1; Sequence=Displayed;
Name=2; Synonyms=H3S;
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEHSR.
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                          TISSUE SPECIFICITY.
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                                                                                                                                                               VQPHGSLEQCWK -> CVERLGKLEASLLLPIWMFSGRWRR
RKHVCBLDVPWMFNQERQNCRGARGWIGRCGLPRPPPSVLQ
LPAEPRQLLLPAPPFGLGRWPCPACFVCTIRIWGWVVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Katsumoto M., Matsumoto S., Saito T., Kambhara M., Takasaki J., Matsushime H., Furuichi K.; Obishi T., Soga T., Matsushime H., Furuichi K.; Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                               /FIId=VSP 001887.
Missing (In isoform 3 and isoform 4).
/FIId=VSP 001888.
WYETSFWLLWANSAVNPULYPICHYSPRRAFFKLLCPDKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
(in isoform 2). (POTENTIAL). ;p 001887.
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                                                                                                                                                                                                                                                                                                                                    Length 445;
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InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1. EPCR_Rhodpsn.
PRINTS; PR01533; GFCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS020237; GPCRHODOPSN.
PROSITE; PS50262; GPROTEIN RECEP_FI_1; FALSE_NEG.
PROSITE; PS50262; GPROTEIN RECEP_FI_2; 1.
PROSITE; PS50262; GFROTEIN RECEP_FI_2; DPCREIN RECEP_FI_2; 1.
PROSITE; PS50262; GFROTEIN RECEP_FI_2; 1.
PROSITE; PS50262; GFROTEIN RECEP_FI_2; 1.
PROSITE; PS50262; GFROTEIN RECEP_FI_1; FALSE_NEG.
PROSITE; PS50262; GFROTEIN RECEP_FI_1; FALSE_NEG.
PROSITE; PS50262; GFROTEIN RECEP_FI_1; FALSE_NEG.
PROSITE; PS50262; GFROTEIN RECEP_FI_1; FALSE_NEG.
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PROSITE; PS50262; GFROTEIN RECEP_FI_1; FALSE_NEG.
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/FTId=VSP 001889.
63DFEFCZ1758FESB CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CystrR2) (RSBPT32).
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CYTOPLASMIC (POT
4 (POTENTIAL).
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100.0%; Pred. No. ...
0; Mismatches
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RN [2]
RN SQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA GAZZAKI Y., FULTON M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA OKAZZAKI Y., PULTON M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA OKAZZAKI Y., PULTON M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA OKAZAKI Y., PULTON M., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Faldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matuada H., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanapin A., Matuada H., Batalov S., Beisel K.W.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanaj A., Kurochkin I. V., Lee Y., Lenhard B., Lyons P.A.,
RA Kanaj A., Kurochkin I. V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlested C., Serple C.A., Settou M., Shimada K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang E.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa R.
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8K458; Q80XQ0; Q8BIR4;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Prokineticin receptor 2 (PK-R2) (G protein-coupled receptor 73-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                          Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                        .67 N-LINKED (GLCNAC. . .) (PC
35507 MW; A122AC8177879D56 CRC64;
                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                            S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                (POTENTIAL) .
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100.0%; Pred. No. v.
0; Mismatches
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Best Local Similarity
Lov.
9, Conservative
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           187
208
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309 AA;
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                                                                                                                                                                                                                                                             166
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STRAIN=CS7BL/6; TISSUE=Brain;

X MEDLINE=22388257; PubMed=12477932;

A Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhath N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Broak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schrertield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schrertion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration the Ewebean the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                     Birney B., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the G(q) subclass of heteromeric G proteins. Activation leads to mobilization of calcium, stimulation of phosphoinositide turnover and activation of p44/p42 mitogen-activated protein kinase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothalamic nucleus, paratenial thalamic nuclei, paracentral halamic nucleus, lateral habenular nucleus, lateral septal nucleus, lateral globus pallidus and amygdala. Highest expression seen in paraventricular thalamic nuclei and is also extensively syptessed in the suprachiasmatic nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in several regions of the brain, including paraventricular hypothalamic nucleus, dormal medial
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF480279; AAM49571.1; -
EMBL; AK030458; BAC26971.1; ALT_INIT.
EMBL; AK030458; BAC26971.1; ALT_INIT.
EMBL; AK080980; BAC30994.1; -
EMBL; AK080980; BAC3108.1; -
EMBL; BC043116; AAM441316.1; -
EMBL; BC043116; AAM441316.1; -
EMBL; BC043116; AAM441316.1; -
EMBL; BC04316; AEM441316.1; -
EMBL; BC04316; AEM441316.1; -
InterPro; IFR00027; GPCR_Rhodpsn.
R Pf0001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
R PROSITE; PS00237; GPCRHODOPSN.
R PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
W G-protein coupled receptor; Transmembrane; Glycoprotein.
ENTRACEBLUIAR (POTENTIAL).
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2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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86
107
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154
168
189
                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;

X MEDLINE=22050031; PubMed=12054613;

A Masuda Y., Takatra Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,

RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,

RT "Isolation and identification of EG-VEGF/prokineticins as cognate
I igands for two orphan G-protein-coupled receptors.";

RT "Isolation and identification of EG-VEGF/prokineticins as cognate
I ligands for two orphan G-protein-coupled receptors.";

RT Blochem. Blophys. Res. Commun. 293:396-402(2002).

CG G(G) subclass of heteromeric G proteins. Activation leads to
mobilization of calcium, stimulation of phosphoinositide turnover

G(G) subclass of heteromeric G proteins. Activation leads to
mobilization of calcium, stimulation of phosphoinositide turnover

G(G) subclass of heteromeric G protein.

CC and activation of p44/p42 mitogen-activated protein kinase (By
CC similarity).

CC -1 SUBCELLUIAR LOCATION: Integral membrane protein.

CC -1 TISSUB SPECIFICITY: Abundantly expressed in the CNS and
crepbellum, testis and ovary.

CC -1 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                              6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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0
                                                                                                                                                                                                                                   205 BY SIMILARITY.
244 S -> P (IN REF. 3).
375 V -> L (IN REF. 2; BAC26971).
43375 MW; 1981FD101324166D CRC64;
                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
          EXTRACELLULAR (POTENTIAL).
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INTERPRO, IPRO00276, GPCR_Rhodpsn.
PRIMT, PR00027; GPCRRHODOPSN.
PROSITE; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS00262; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                             Query Match
2.3%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 0.4
Matches 9; Conservative 0; Mismatches
                                   (POTENTIAL)
                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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241
270
291
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244
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221
242
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332
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375
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ID PKR2 RAT
AC Q8R415;
DOMAIN
TRANSMEM
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PKR2_HUMAN
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DT_10-OCTION
DD_10-OCTION
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-- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the GG subclass of heteromeric G proteins. Activation leads to GG subclass of heteromeric G proteins. Activation leads to and activation of calcium, stimulation of phosphoinositide turnover and activation of p44/p42 mitogen-activated protein kinase (By similarity).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Prokineticin receptor 2 (FK-R2) (G protein-coupled receptor 73-like 1)
(G protein-coupled receptor 15E).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
          EXTRACELLULAR (POTENTIAL)
                                                                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                (POTENTIAL).
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o. 0.41;
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100.0%; Pred. No. 0.4
tive 0; Mismatches
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"Identification and molecular characterization of two closely related g protein-coupled receptors activated by prokineticins/endocrine gland vascular endothelial growth factor."; J. Biol. Chem. 277:19276-19280(2002).
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10-OCT-2003 (Rel. 42, Last annotation update)
Prokineticin receptor 2 (PK-R2) (G protein-coupled receptor 73-like 1)
(GPR92) (GPR92).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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Lin D.C.-H., Bullock C.M., Ehlert F.J., Chen J.-L., Tian H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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5. 0.41;
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Q8NFJG; Q9NTTO;
10-OCT-2003 (Rel. 42, Created)
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9; Conservative
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    PROSITE; PS00237;
PROSITE; PS50262;
G-protein coupled
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A Griffiths G., Griffiths M.N.D., Gwilliam R., Hall R.E.,
A Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
A Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
A Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
A Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
A marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
A mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Stoce C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Swunn R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
R Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Porers T.
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Nature 414:865-871(2001).

-!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the G(q) subclass of heteromeric g proteins. Activation leads to mobilization of calcium, stimulation of phosphoinositide turnover and activation of p44/p42 mitogen-activated protein kinase.
-!- SUBCELULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in the ileocecum, thyroid gland, pituitary gland, salivary gland, adrenal gland, testis, ovary and

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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Ffam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHDDDSN.
PROSITE; PS02237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-Protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 54
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EMBL; AB084081; BAC24022.1; -.
EMBL; AL121755; CAB89854.1; ALT_SEQ.
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DB 1; Length 384;

Score 9; D Pred. No.

2.3%; S 100.0%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                              MEDLINE=22050031; PubMed=12054613; Manual Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Pointo M.; Teolation and identification of EG-VEGF/prokineticins as cognate ligands for two orphan G-protein-coupled receptors."; Blochem. Biophys. Res. Commun. 293:396-402(2002).

-I-FUNCTION: Receptor for prokineticin I. Exclusively coupled to the G(q) subclass of heteromeric G proteins. Activation leads to mobilization of calcium, stimulation of phosphoinositide turnover
                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bosimae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                          and activation of p44/p42 mitogen-activated protein kinase (By
                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)
G protein-coupled receptor ZAQ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL),
N-LINKED (GLCNAC. .) (POTENTIAL),
N-LINKED (GLCNAC. .) (POTENTIAL),
N-LINKED (GLCNAC. .) (POTENTIAL),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 63 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY089972; AAM1888.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
253
228
303
322
343
393
11
14
36
                                                                                                                                                        Bos taurus (Bovine).
             PKR1 BOVIN
ID PKR1 BOVIN
                                          QBSPNZ;
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TRANSMEM
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TRANSMEM
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CARBOHYD
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RESULT 11
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Matches

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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                   PROSITE; PS00237; G_PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0D36461CA99CAEC1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 9; DB 1;
100.0%; Pred. No. 0.42;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IS -> MT (IN REF
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     InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44769 MW;
                                                                  PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 417:405-410(2002)
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J. Biol. Chem. 277:19276-19280(2002)
J. Biol. Chem. 277:19276-19280(2002)
J. FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the cid subclass of heteromeric G proteins. Activation leads to mobilization of calcium, stimulation of phosphoinositide turnover and activation of p44/p42 mitogen-activated protein kinase.
J. SUBCELULUAR LOCATION: Integral membrane protein.
TISSUB SPECIFICITY: Expressed in the stomach, throughout the small intestine, colon, rectum, thyroid gland, pituitary gland, salivary gland, adrenal gland, testis, ovary, brain, spleen, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22050031; PubMed=12054613; Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Tukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Fujino M.; Iliatomi N., Ohtaki T., Onda H., Fujino M.; Iliganda for two orphan G-protein-coupled receptors."; Hiochem. Biophys. Res. Commun. 293:396-402(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=22314729; PubMed=12427552; Soja T., Hiyama H., Takasaki J., Soja T., Matsumoto S.-I., Oda T., Saito T., Hiyama H., Takasaki J., Kamohara M., Ohishi T., Matsushime H., Furuichi K.; Molecular cloning and characterization of prokineticin receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       OSTOROGY; OSNRUT; 10-OCT-2003 (Rel. 42, Created) 110-OCT-2003 (Rel. 42, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) Prokineticin receptor 1 (PK-R1) (G process)
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0
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                                                               Length 393;
                                                                                                                        0; Indels
           CF302DD364D8A2CC CRC64;
                                                               2.3%; Score 9; DB 1;
100.0%; Pred. No. 0.42;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1579:173-179(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GPR73a) (G protein-coupled receptor ZAQ). GPR73 OR PKR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22028034; PubMed=11886876;
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                 44602 MW;
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                         NLAISDFLV 111
                                                                                                                                                                                     56 NLAISDFLV 64
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                                                                                                       Local Similarity
                         393 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         PKR1 HUMAN
                                                                                                                                                                                                                                              103
                         SEQUENCE
                                                                          Query Match
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. ARREST REPRESENTATE BEST STANDER STA

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Gaps

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Length 393; 0; Indels

3

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-i- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the G(q) subclass of hereromeric G proteins. Activation leads to mobilization of calcium, stimulation of phosphoinositide turnover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20225484; PubMed=10766665;
MEDLINE=20225484; PubMed=1076665;
MEDLINE=20225484; PubMed=1076665;
Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
Grawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
organisation and assignment to human chromosome 11q21.1 and 2p14 and mouse chromosome 9 and 6.";
Biochim. Biophys. Acta 1491:369-375(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6;
MEDLINE=22022134; PubMed=12024206;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Cheng M.Y., Lealie F.M., Zhou Q.-Y.;
Weaver D.R., Leslie F.M., Zhou Q.-Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the suprachiasmatic nucleus.";
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                     10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)
393 AA.
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344
11
137
393 AA;
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SEQUENCE FROM N.A.
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233
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304
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OPSD_CAMAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
        similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expessed at high levels in the heart, skeletal
muscle and pandreas. Expressed at lower levels in the brain, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley;
MEDLINE=22050031; PubMed=12054613;
Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                      SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
and activation of p44/p42 mitogen-activated protein kinase (By
                                                                                                                                                                                                                                                                                                                                                                    7 (POTENTIAL).
CYTODELASMIC (POTENTIAL).
N'-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)
(G protein-coupled receptor ZAQ).
                                                                                                                                                                                           Pfam; PFUNDU1; /Lul 1, CEGRADODESN.
PRINTS; PRO0237; GPCRRADODESN.
PROSITE; PSO1267; GPROTEIN_RECEP_F1_2; 1.
PROSITE; PSO1262; GPROTEIN_RECEP_F1_2; 1.
CATABGE 1 62 EXTRACELLULAR (POTENTIAL).
DOMAIN 63 83 1 (POTENTIAL).
DOMAIN 84 98 CYTOPLASMIC (POTENTIAL).
TRANSMEM 99 119 2 (POTENTIAL).
DOMAIN 120 146 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                         3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 9;
                                                                                                                                                                     MGD; MGI:1928676; Gpr73.
InterPro; IPR000276; GPCR_Rhodpsn.
PFam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                               EMBL; AF236082; AAF43706.1; -. FMRI; AF487278; AAM49570.1; -.
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ММ
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167
179
200
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                                                                                                                                                                                                                                                                                                                                                                  343
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                                                                                                                                                                                                                                                                                                                                                                                     11
137
393 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q8R416;
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0
                                                                                                                                                                                                                                            similarity).
SUBCELULUAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed in peripheral tissues with the highest level in the splean and moderate levels in the adipose tissues, thymus, lung, kidney, testis, uterus and small intestine.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Inatomi N., Ohtaki T., Onda H., Fujino M.;
"Isolation and identification of EG-VEGF/prokineticins as cognate
"Isolation and identification of EG-VEGF/prokineticins as cognate
ligands for two orphan G-protein-coupled receptors.";
Blochem. Biophys. Res. Commun. 293:396-402(2002).
-!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the
G(q) subclass of heteromeric G proteins. Activation leads to
mobilization of calcium, stimulation of phosphoinositide turnover
and activation of p44/p42 mitogen-activated protein kinase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
Formicidae; Formicinae; Camponotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
S (POTENTIAL).
C YTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7Fm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; GFRCHODOPSN.
PROSITE; PS00237; GFRCHEIN RECEP_F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 393; 0.42;
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EXTRACELLULAR (POTENTIAL)
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2 (POTENTIAL)
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.3%; Scc...
100.0%; Pred. No. c...
0; Mismatches
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CYTOPLASMIC (
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103 NLAISDFLV 111
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                                                 INTERPO, IPRO0176; GPCR_Rhodpsn.
InterPro; IPR00176; Opsin.
Pfam, PR001017; Ttm 1; 1.
PR00176; PR0023; GPCRHDODPSN.
PROSITE; PS0023; GPCRIN RECEP_F1_1; 1.
PROSITE; PS0023; GPCRIN RECEP_F1_2; 1.
PROSITE; PS0023; OFPINI RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PROMAIN IN S3
TISSUE=Retina;
MEDINIE=89803419; PubMed=9372150;
MEDINIE=8903419; PibMed=9372150;
Popp M.P., Grisshammer R., Hargrave P.A., Smith W.C.;
Papp M.P., Grisshammer R., Hargrave P.A., Smith W.C.;
Papp opsins: sequences from the Saharan silver ant and the carpenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.0%; Score 8; DB 1; Length 378; Best Local Similarity 100.0%; Pred. No. 4.3; Matches 8; Conservative 0; Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL)
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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378 AA;
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Search completed: October 1, 2004, 10:26:53 Job time: 27 secs

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Gaps

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Query Match
Best Local Similarity
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091zy3 cavia porce
0961d9 homo sapien
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pseudomonas
                                            1, 2004, 10:20:40 ; Search time 118 Seconds
(without alignments)
1045.488 Million cell updates/sec
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canis famil
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Q8ni49
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Q8ni50
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                             OM protein - protein search, using sw model
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Q91ZY1
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Q96LD9
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sp_bacteria:*
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sp_human:*
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sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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sp rodent:*
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Match Length DB
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951160	Q871W9	Q8YDR4	QBFUN6	Q98JZ0	Q8E3K3	Q8DXY4	020759	043153	Q7WD90	Q7W5Q4	Q7VW94	052293	088P	Q9RYQ3	Q7WJ42	Q94HB1	0574	Q94D59	986198	Q8E9K4	Q8IES7	Q8YNG1	Q866B5	QSTDP	QSTDP6	QBH1V0	O8YXH9	Q8PZ	AL
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181	278	281	281	292	314	314	328	368	396	396	396	400	400	426	457	527	534	672	902	1188	9271	55	72	80	82	93	96	100	
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17	18	19	20	21	22	23	24	25	56	27	58	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

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STEALNIBALE ACCEPTOR.

A LIU C., Wilson S., Kuei C., Lovenberg T.W.;

LIU C., Wilson S., Kuei C., Lovenberg T.W.;

T. "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
ST "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
ST "Submitted (MAR-2001) to the EMBLGGenBank/DDBJ databases.

SUBMITTER ELOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR MGD; MGI:2429635; Hrh4.

MGD; MG:01005837; C:integral to plasma membrane; IC.

GO; GO:0005837; C:integral to plasma membrane; IC.

GO; GO:0004969; F:histamine receptor activity; IDA.

InterPro; IPR000276; GPCR Rhodpsn.

PRINTS; PR001276; HSTAMINERAR.

PRINTS; PR01226; HSTAMINERAR.

PRINTS; PR01226; HSTAMINERAR.
                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59EC73CB5214C5E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1, 1.
PROSITE; PS50263, G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN COUPLED G_FCEPLOT; Transmembrane.
SEQUENCE 391 AA; 44248 MW; S9EC73CB5214CSEO CRCC
                                                                                                    Last sequence update)
Last annotation update)
   391 AA
                                                                     Created)
   PRT;
                        Q91ZY2;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
PRELIMINARY;
                                                                                                                                                              Histamine H4 receptor.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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96.9%; Score 379; DB 11; Length 391; 100.0%; Pred. No. 0;

Matches

g ð 임 à

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EQUENCE FROM N.A.

SEQUENCE FROM N.A.

Ind. ("Mison S., Kuei C., Lovenberg T.W.;

Ind. ("Comparison of human, mouse, rat, and guinea pig histamine H4 receptor "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

- SIMILARITY: BELONGS TO FAMILY 1 OF G-ROTEIN COUPLED RECEPTORS.

REMBL; AR358858; AAK97379-1; -...

ROJ GO:0004872; F:receptor activity; IEA.

ROJ GO:0004872; F:receptor activity; IEA.

ROJ GO:0007186; F:receptor activity; IEA.

ROJ GO:0007186; F:receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity IEA.

ROJ GO:0007186; F:Receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity; IEA.

ROJ GO:0007186; F:Receptor activity; IEA.
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Nguyen T., George S.R., Lee D.K., Cheng R., Lynch K.R., O'Dowd B.F.;

"Discovery of H4, a Novel Histamine Receptor.",

"Discovery of Engly a Novel Histamine Receptor.",

submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                          Histanine H4 receptor.

Cavia porcellus (Guinea pig).

Bukaryota; Metazoa (Guinea pig).

Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

NCBI_TaxID=10141;
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PROSITE, PS50262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 389 AA; 44511 MW; 51AF32FD6FIC3E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 1.4e-24;
tive 0; Mismatches 0;
131 KIVAQMVAVWILAFLVNGPMILASDSWKNSTNT 163
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                                                                                                                                                             PRT;
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Q91ZY3
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                                                                         1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS 60
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STRAIN=Sprague-Dawley;
STRAIN=Sprague-Dawley;
Liu C., Wilson S., Kuei C., Lovenberg T.W.;
"Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation.";
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
-! - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-! - SUBCELLULAR: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR008102; Histamine_H4.
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PRINTS, PRO1726; HISTAMINEH4R.
PROSITE; PSO0237; GPOTYBIN RECRE F1.1; 1.
PROSITE; PSSO026. GPROTEIN RECRE F1.2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEGUENCE 391 AA; 44023 MW; C707BA6E39GFED41 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 1.3e-25;
0; Mismatches 0;
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                         0; Mismatches
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ilarity 100.0%; Pr
Conservative 0;
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                         379; Conservative
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Best Local Similarity
Matches 33; Conserv
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RESULT 2 Q912Y1

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EMBL; AF346903; AAM43828.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004969; F:histamine receptor activity; IEA.
GO; GO:0004891; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; F:rhodopsin-like receptor protein signalin...; IEA.
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Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                     Witte D.G., Esbenshade T.A., Hancock A.A., Yao B.B.;
"The canine histamine receptor H3 (HRH3) partial cDNA sequence.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weiner D.M.;
"Molecular Cloning and Characterization of Functionally Distinct
Isoforms of the Human Histamine H3 Receptor.";
Neuropharmacology (2002)
               Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 11; DB 6; Length 147;
100.0%; Pred. No. 0.0074;
iive 0; Mismatches 0; Indels
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147 AA; 16900 MW; 67F6A741B518B54E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Histamine H3 receptor isoform 5.
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Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 11; Conservative 0; Mismatches 0;
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InterPro; IPR003980; H3 receptor.
Prim; PR0001; 7tm 1; 1.
PRINTS; PR00177; GERRANDERS.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 1; 1.
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                                                                  SEQUENCE FROM N.A.
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                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                  Receptor.
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NON TER
SEQUENCE
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Q8N150;
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:d-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodopsn.

Pfam; PF00001; 7fm 1; PR00001; 7fm 1: PRINTS; PR00277; GPCRRHODOPSN.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01726; HISTAMINEHAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.;
"CDNA cloning and characterization of porcine histamine H4 receptor.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRH3.
Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                 5.4%; Score 21; DB 4; Length 390;
.00.0%; Pred. No. 5.3e-13;
.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.1%; Score 16; DB 6; Length 390; 100.0%; Pred. No. 9.7e-08; tive 0; Mismatches 0; Indels
             Pfam, PP00001, 7tm 1, 1.

PRINTS; PR00237; GPCRRHODDPSN.

PRINTS; PR01726; HISTAMINEH4R.

PROSITE; PS00262; GPROTEIN RECEP F1 1, 1.

PROSITE; PS05062; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 390 AA; 44469 MW; CCG2B5D30D216C66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC8FD363A6F44D3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TIEMBLrel. 24, Created)
01-JUN-2003 (TIEMBLrel. 24, Last sequence update)
01-OCT-2003 (TIEMBLrel. 24, Last sequence update)
Histamine receptor H3 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                         390 AA
                                                                                                                                                                              Best Local Similarity 100.0%; Fred. No. 5.3
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA.
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                     93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                                                                                                         93 TDYLLCTASVYNIVLISYDRY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
InterPro; IPR008102; Histamine_H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 DYLLCTASVYNIVLIS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 DYLLCTASVYNIVLIS 111
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine H4 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=9823;
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                                                                                                                                                                 Query Match
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RESULT 6
0865E3
1D 0865)
AC 01-07
DT 01-07
DT 01-07
DT Hist.
GN HRH3
OC EUKA

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EMBL; AF346904; AAM43829.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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SEQUENCE
                                                                                                                                                                      Receptor.
SEQUENCE
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Q8WXZ9
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Weiner D.M.;

"Molecular Cloning and Characterization of Functionally Distinct

"Molecular Cloning and Characterization of Functionally Distinct

Suboforms of the Human Histamine H3 Receptor.";

Submitted (MOV-2000) to the BMBL/GenBank/DDBJ databases.

EMBL; AF321912; AAL71913.1;

EMBL; AF321912; AAL71913.1;

EMBL; AF321912; AAL71913.1;

GO, GO:00016021; Finceptor activity; IEA.

GO, GO:0004872; Fincecptor activity; IEA.

GO, GO:000188; Fincheptor activity; IEA.

GO, GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR00376; H3_receptor.
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Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                   TISSUE=Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weiner D.M.; "Moleoular Cloning and Characterization of Functionally Distinct "Moleoular Cloning and Histamine H3 Receptor."; Isoforms of the Human Histamine H3 Receptor."; Neuropharmacology 0:0-0(2002).
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2.8%; Score 11; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                    OFFICE, 1002 (TrEMBLrel. 20, Created) 01-MR-2002 (TrEMBLrel. 20, Last sequence update) 01-MR-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                            301 AA
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PRINTS; PR00237; GPCRRHODOSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 INLAISDFLVG 65
                                                                                                                PRELIMINARY;
                        65
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74 INLAISDFLVG 84
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                        55 LNLAISDFLVG
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                        RESULT 8
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Wolecular Cloning and Characterization of Functionally Distinct

"Molecular Cloning and Characterization of Functionally Distinct

Isoforms of the Human Histamine H Receptor.";

Submitted (NOV-2000) to the EMBL, GenBank/DDBJ databases.

EMBL, AF321911; AAL71912.1;

EMBL, AF321911; AAL71912.1;

GO, GO:0016221; Ciintegral to membrane, IEA.

GO, GO:00048672; Finistamine receptor activity; IEA.

GO, GO:0001884; Finistamine receptor activity; IEA.

GO, GO:0001884; Finistamine receptor activity; IEA.

GO, GO:0001886; Finistamine receptor activity; IEA.

InterPro; IRR000276; GPCR Rhodpsn.

InterPro; IRR000276; GPCR Rhodpsn.

InterPro; IRR000376; H3_receptor.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004962; F:intetamine receptor activity; IEA.
GO; GO:0004972; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor protein signalin. . .; IEA.
GO; GO:000186; P:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR003980; H3_receptor.
Ffam; PF00001; 7tm 1, 1.
PRINTS; PR01471; HSTAMINBH3R.
PRINTS; PR01471; HSTAMINBH3R.
PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
2.8%; Score 11; DB 4; Length 309
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA; 34242 MW; B7496F7D1D2A206B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NAR-2002 (TrEMBLrel. 20, Created)
01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Histamine H3 receptor isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
... 0; Mismatches
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 100.
Matches 11; Conservative
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PRINTS; PR00237; GPCRRHODDPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1: 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2: 1.
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                                                                                                                                                                                                                                                                                                                        PRT;
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Mol. Biol. Evol. 20:633-643(2003).
EMBL; AX117084; AAM78203.1; -.
NON TER
                                                                                            445 AA; 48591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feng Y.M., Yeo C.C., Poh C.L.;
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                                                                                                                                                               11; Conservative
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                                                                                                                                             Similarity
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STRAIN=NCIB 9867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=47615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001
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01-JUN-2002
                                                                           Receptor.
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                                                                                                                             Query Match
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                                                                                                                                               Local
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                                                                                                                                                               Matches
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AY231164, AA0633757.1;
GO: 00.16021; C.integral to membrane; IEA.
GO; GO: 0004969; F: histamine receptor activity; IEA.
GO; GO: 0004872; F: receptor activity; IEA.
GO; GO: 0001584; F: receptor activity; IEA.
GO; GO: 000188; P: Proposin-like receptor activity; IEA.
GO; GO: 0007186; P: Protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004969; E:histamine receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-procein coupled receptor protein signalin. .; IEA.
InterPro; IPR00296; GPCR_Rhodops.
InterPro; IPR003980; H3_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                      TISSUE=Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                     "Molecular Cloning and Characterization of Functionally Distinct Isoforms of the Human Histamine H3 Receptor.", Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AA; 41570 MW; FAE9DFC5C3AF4DE9 CRC64;
                              01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Histamine H3 receptor isoform 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
   373 AA
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
 PRT;
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PRINTS; PR01471; HISTAMINEH3R.
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Best Local Similarity 100.
Matches 11, Conservative
PRELIMINARY;
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NCBL_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm 1; 1
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                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      Weiner D.M.;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypioides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22569057; PubMed=12679546;
Senchina D.S., Alvarez I., Cronn R.C., Liu B., Rong J., Noyes R.D., Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.F.;
"Rate variation among nuclear genes and the age of polyploidy in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of gentisate 1,2-dioxygenase from Pseudomonas alcaligenes NCIB 9867."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF173167; AAG19456.1; InterPro; IPR002559; Transposase 11. Pfam; PF01609; Transposase_11; 1.
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Pseudomonadaceae; Pseudomonas.
                                                 2.8%; Score 11; DB 6; Length 445;
100.0%; Pred. No. 0.02;
Live 0; Mismatches 0; Indels
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E79440A4EC09CA8C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative root hair defective 3 protein (Fragment).
Gossypioides kirkii.
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Last annotation update)
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2.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 6.1
Matches 8; Conservative 0; Mismatches
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MisDLINE-21164917; PubMed=11230166;

Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,

Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,

Ansorge W., Desterhoeft A., Beyer A., Koehrer K., Strack N.,

Mewes H.W., Oterwaelder B., Obermaier B., Tampe J., Heubner D.,

Wambutt R., Korn B., Klein M., Poustka A.;

Thyarda a Catalog of Human Genes and Proteins: Sequencing and

Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Straubberg R.;
Straubberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL13659, CAB66485.1;
EMBL; BC03942; AAH39242.1;
Hypothetical protein.
EMBL BROWNER 181 AA; 19997 MW; A73A03FD0C3B3FBB CRC64;
                                                                                  Length 150;
                                                                                                                                                    0; Indels
150 AA; 17439 MW; 8AAC59D07FD6E83B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Brain cell membrane protein 1)
DKFZP761J17121.
                                                                          Ouery Match
2.0%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches
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               SEQUENCE
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